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Database
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Listing first 45 summaries
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                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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ALIGNMENTS

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82.4	83.7	83.7	84.3	85.1	85.1	85.1	85.3	88.8	89.4	90.6	91.0	95.4	97.1	99.1	99.1	99.9	99.9	100.0	Match	Query
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Query Match Best Local Similarity

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34.9	35.0	35.5	41.0	41:0	41.0	42.5	47.4				56.6	59.6	59.7	66.1	66.5	71.6	71.6	71.6	74.6	74.6	75.7	75.7	80.6	80.6	80.6
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REFERENCE AUTHORS TITLE JOURNAL LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM ORIGIN FEATURES CDS Bource Obendorf,M. and Wolf,S. Modulation of the activity of nuclear receptors via EWS Patent: EP 1455190-A 1 08-SEP-2004; Schering Aktiengesellschaft (DE) CQ867364 2390 bp Sequence 1 from Patent EP1455190. CQ867364 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Homo sapiens Homo sapiens (human) CQ867364.1 GI:51997589 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606" 44._.2014 MISNRGGLPPREGRAWPPLRGGPGGPGGPGGPMGRAGGRGGDGGPPPRGPRGSRGN PSGGGNVQHRAGDWQCPNPGCGNQNFAWRTECHQCKAPKPEGFLPPPFPPPGGPRGR GPGCMRGGRGGLMDRGGPGGMPRGGRGGDRGGPRGGRCMDRGGFGGGRRGGPGGPGGP VYGQESGGFSGPGENRSMSGPDNRGRGRGGFDRGGMSRGGRGGRGGMGSAGERGGFN KPGGPMDEGPDLDLGPPVDPDEDSDNSAIYVQGLNDSVTLDDLADFFKQCGVVKMNKR TGQPMIHIYLDKETGKPKGDATVSYEDPPTAKAAVEWFDGKDFQGSKLKVSLARKKPP LMEQMGGRRGGRGGPGKMDKGEHRQERRDRPY" note="unnamed protein product" Location/Qualifiers DNA linear PAT 13-SEP-2004

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Qy 241 TGCAACTTCTTATGGACAGCCTCCCACTGGTTATACTACTCCAACTGCCCCCAGGCATA 300	61 CAGTACCTATAGCCAAGCTGCAGGCATATGGGCAACCTATGGACA 1	Query Match 99.9%; Score 2388.4; DB 6; Length 2390; Best Local Similarity 100.0%; Pred. No. 0; Matches 2389; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Qy 1 AGAGGAGACGGACGTTGAGAGAAACGAGGAGGAGAGAAAATGGCGTCCACGGATTA 60	FEATURES GENE LOGIC INC (US) FEATURES LOCATION/Qualifiers Source 12390 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606" /note="EMBL/GenBank Accession No. X66899" ORIGIN		RESULT 2 AX411125 LOCUS AX411125 DEFINITION Sequence 3772 from Patent WO0229103. ACCESSION AX411125 VERSION AX411125.1 GI:21443830	Db 2281 GTGGAGAACCAAGAGGGCCTCTTAACTGTAACAATGTTCATGGTTGTGATGTTTTTTTT	Qy 2221 AAAAATGGTTGTTTAAGACTTTAACAATGGGAACCCCTTGTGAGCATGCTCAGTATCATT 2280	Oy 2161 GAAGAAACATTAAAACAAGTTAAATGGTAGTGTGGGGAGTTTTTTTT
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                       Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Gene fusion with an ETS DNA-binding translocation in human tumours
Nature 359 (6391), 162-165 (1992)
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 TCAAGGATATGCACAGACCACCCAGGCATATGGGCAACAAAGCTATGGAACCTATGGACA
             TCAAGGATATGCACAGACCCACCCAGGCATATGGGCAACAAAGCTATGGAACCTATGGACA
                                             CAGTACCTATAGCCAAGCTGCAGCGCAGCAGCAGCCTACAGTGCTTACACCGCCCAGCCCAC
                                                          CAGTACCTATAGCCAAGCTGCAGCGCAGCAGGGCTACAGTGCTTACACCGCCCAGCCCAC
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/evidence=experimental
2371
/gene="EWS"
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/gene="EWS"
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/mol type="mRNA"
/db_xref="taxon:9606"
/chromosome="22q12"
/clone="BF1AC5"
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/clone_Tib="cDNA, Stratagene 936206"
/dev_stage="foetus"
1. .2390
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2350. .2355
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                                                                                                                                            99.9%; Score 2388.4;
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tive 0; Mismatches
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2281 GTGGAGAACCAAGAGGGCCTCTTAACTGTAACAATGTTCATGGTTGTGATGTTTTTTTT		1201 TGTTAAGATGAACAAGAGAACTGGGCAACCCATGATCCACATCTACCTGGACAAGGAAAC	• •
	Qy AGCAGTGTGGGGT 1200 AGCAGTGTGGGGT 1200	1141 AGGATTAAATGACAGTGTGACTCTAGATGATCTGGCAGACTTCTTTAAGCAGTGTGGGGT	0 1
GAAGAAACATTAAAACAAGTTAAATGGTAGTGCCGGACTTTTTTTCTTCCTTC	DAATTTATGTACA 1140 CAATTTATGTACA 1140 Db	1081 TGATCTAGGCCCACCTGTAGATCCAGATGAAGACTCTGACAACAGTGCAATTTATGTACA	0 \
ATGTTGGCCACACATTATGATTATCCTTGTCTGTACTTAGTATTTTTCACCATTTGT	ANGGACCAGATCT 1080	1021 CGCTGGAGAGCGAGGTGGCTTCAATAAGCCTGGTGGACCCATGGATGAAGGACCAGAT	0 \
GACTACCAGATTTATTTTAAACCAGAAAATGTTTTAAATTTATAATTCCATATTTATA	1020	961 ATTTGATCGTGGAGGCATGAGCAGAGGTGGGCGGGGAGGAGGACGCCGGTGGAATGGGCAG	0 ~
GCACCGTCAGGAGCGCACAGATCGGCCCTACTAGATGCAGAGACCCCGCAGAGCTGCATT	960	901 CGGACCAGGAGAGAACCGGAGCATGAGTGGCCCTGATAACCGGGGCAGGGGAAGAGAGGGGGG	0 1
ZI GGAACAGAIGGGAGGAIGAAGAGGACGIGGAGGAACTGGAAAAATGGATAAAGGCGA	900	841 ATTCCGACAGGACCACCCCAGTAGCATGGGTTTTATGGGCAGGAGTCTGGAGGATTTTC	0 \
61 CCGAGGTGGCTTTGGTGGAGGAAGAACGAGGTGGGCCCTGGGGGGCCCCTGGACCTTTGAT 61 CCGAGGTGGCTTTGGTGGAGGAAGAACGAGGTGGCCCTGGGGGGCCCCCTGGACCTTTGAT	840	781 CTACAGCCAAGCTCCAAGTCAATATAGCCAACAGAGCAGCAGCTACGGGCAGCAGAGTTC	0 \
ATTITCAGAGGTGGCCGTGGTGGACACAGAGTGGCTTCCGTGGTGGCCGGGGATGGA	780	721 TGGTCAACAAAGCAGCTATGGGCAGCAGCACCCACTAGTTACCCACCC	0 \
TGGCCCTGGTGGCATGCGGGGAGGAAGAGGTGGCCTCATGGATCGTGGTGGTCCCGGTGG	720	661 CAGTTACTCTCAGCAGAACACCTATGGGCAACCGAGCAGCTATGGACAGCAGAGTAGCTA	0 ~
AAAGCCTGAAGGCTTCCTCCCGCCACCCTTTCCGCCCCCGGGTGGTGATCGTGGCAGAGG	660	601 ACCTCCATCCTACCCTCCTACCAGCTATTCCTCTACACAGGCCGACTAGTTATGATCAGAG	0 <
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61 AGGGAACCCCTCTGGAGGAGGAAACGTCCAGCACCGAGCTGGAGACTGGCAGTGTCCCAA	540	481 TGAGACTAGTCAACCTCAATCTAGCACAGGGGTTACAACCAGCCCAGCCTAGGATATGG	0 <
01 CATGGGAGGCCGTGGAGGAGATAGAGGAGGCTTCCCTCCAAGAGGACCCCGGGGTTCCCG 1	DAAACAAGCCCAC 480 	421 CTATGGGCAGCAGCCAGCCACTGCACCTACAAGACCGCAGGATGGAAACAAGCCCAC	0 <
41 GCCACCACCACTCCGTGGAGGTCCAGGAGGCCCAGGAGGTCCTTGGGGGACCCATGGGTCG 15	420	361 CACCACCCAGGCCTCCTATGCAGCTCAGTCTGCATATGGCACTCAGCCTGCTTATCCAGC	0 <
1381 GAAGAAGCCTCCAATGAACAGTATGCGGGGTGGTCTGCCACCCCGTGAGGGCAGAGGCAT 1440		301 CAGCCAGCCTGTCCAGGGGTATGGCACTGGTGCTTATGATACCACCACTGCTACAGTCAC	0 <
1321 CGTGGAATGGTTTGATGGGAAAGATTTTCAAGGGAGCAAACTTAAAGTCTCCCTTGCTCG 1380	CCCCCAGGCATA 300	241 TGCAACTTCTTATGGACAGCCTCCCACTGGTTATACTACTCCAACTGCCCCCCAGGCATÁ	σ <
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CENTRE NAT RECH SCIENT (FR)
Other publication FR 2691475 931126
Other publication JP 8500964T 960206.
Location/Qualifiers
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1 (bases 1 to 2371)

Aurias,A., Delattre,O., Desmaze,C., Melot,T., Peter,M.,

Plougastel,B., Thomas,G. and Zucman,J.

NUCLEIC ACID CORRESPONDING TO A GENE OF CHROMOSOME 22 INVOLVED IN RECURRENT CHROMOSOMAL TRANSLOCATIONS ASSOCIATED WITH THE DEVELOPMENT OF CANCEROUS TUMORS
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                       TCTAGCACAGGGGGTTACAACCAGCCCAGCCTAGGATATGGACAGAGTAACTACAGTTAT 559
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/mol type="unassigned DNA"
/db_xref="taxon:9606"
/dev_stage="FOETUS"
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Bource	nucleic acids of	Delattre,O., Desmaze,C., N. B., Thomas,G. and Zucman, C., Thomas,G. and Zucman, corresponding to a gene promosomal translocations	Unknown. M Unknown. Unclassified. 1 (bases 1 to 2371)	ION AR080100.1 GI:1000683	AR080100 2371 b	QY 2360 CARATGTTTAATAAAAAAAAAAAAAAAAAAAAA 2390	QY 2300 TCTTAACTGTAACAATGTTCATGGTTGTGATGTTTTTTTT	OY 2240 TITAACAATGGGAACCCCTTGTGAGCATGCTCAGTATCATTGTGGAGAACCAAGAGGGCC 2299	OY 2180 TTAAATGGTAGTGTGCGGAGTTTTTTTTTCTTCCTTCTTTTAAAAATGGTTGTTTAAGAC 2239	QY 2120 GATTATTCCTTGTCTGTACTTTAGTATTTTTCACCATTTGTGAAGAAACATTAAAACAAG 2179	QY 2060 TAAACCAGAAAATGTTTTAAATTTATAATTCCATATTTATAATGTTGGCCACAACATTAT 2119	QY 2000 GATCGGCCCTACTAGATGCAGAGACCCCGCAGAGCTGCATTGACTACCAGATTTATTT	QY 1940 AGAGGAGGACGTGGAGGACCTGGAAAAATGGATAAAGGCGAGCACCGTCAGGAGCGCAGA 1999	QY 1880 GGAAGACGAGGTGGCCCTGGGGGGCCCCCTGGACCTTTGATGGAACAGATGGGAAGA 1939	QY 1820 GGTGGAGACAGAGGTGGCTTCCGTGGTGGCCGGGGCATGGACCGAGGTGGCTTTGGTGGA 1879	QY 1760 GGAGGAAGAGGTGGCCTCATGGATCGTGGTGGTCCCGGTGGAATGTTCAGAGGTGGCCGT 1819	QY 1700 CCGCCACCCTTTCCGCCCCCGGGTGGTGATCGTGGCAGAGGTGGCCCTGGTGGCATGCGG 1759	Db 1621 AACTTCGCCTGGAGAACAGAGTGCAAACAGTGTAAAGGCCTGAAAGCCTGAAGGCTTCCTC 1680
OY 980 AGCAGAGGTGGGCGGGGAAGGACGCGGTGGAATGGGCAAGAGCGAGAGGGAGG	Qy 920 AGCATGAGTGGCCCTGATAACCCGGGGGCAAGAGAGGGGGATTTGATCGTGGAGGCATG 979	QY 860 AGTAGCATGGGTGTTTATGGGCAGGAGTCTGGAGGATTTTCCGGACCAGGAGAGAACCGG 919	Qy 800 CAATATAGCCAACAGAGCAGCAGCTACGGGCAGAGATTCATTC	QY 740 GGGCAGCAGCTCCCACTACTTACCCACCCCAAACTGGATCCTACAGCCAAGCTCCAAGT 799	661	Qy 620 ACCAGCTATTCCTCTACACAGCCGACTAGTTATGATCAGAGCAGTTACTCTCAGCAGAAC 679	OY 560 CCCCAGGTACCTGGGAGCTACCCCATGCAGCCAGTCACCTCCATCCTACCCTTCCT 619	Qy 500 TCTAGCACAGGGGGTTACAACCAGCCCAGCCTAGGATATGGACAGAGTAACTACAGTTAT 559	OY 440 GCCACTGCACCTACAAGACCGCAGGATGGAAACAAGCCCACTGAGACTAGTCAACCTCAA 499	OY 380 GCAGCTCAGTCTGCATATGGCACTCAGCCTATCCAGCCTATGGGCAGCAGCA 439	Qy 320 TATGGCACTGGTGCTTATGATACCACCACTGCTACAGTCACCACCCAGGCCTCCTAT 379	OY 260 CCTCCCACTGGTTATACTACTCCAACTGCCCCCAGGCATACAGCCAGC	QY 200 ACCCAGGCTCAGACCACTGCAACCTATGGGCAGACCTCTTATGGACAG 259	OY 140 ACCCAGGCATATGGGCAACAAAGCTATGGAACGTATGGACAGCCCACTGATGTCAGCTAT 199	Qy 80 GCAGCGCAGCAGGCGTACAGTGCTTACACCGCCCAGCCCACTCAAGGATATGCACAGACC 139	Qy 20 GAGAACGAGGAGGAGGAGAGAAATGGCGTCCACGGATTACAGTACCTATAGCCAAGCT 79	Query Match 99.1%; Score 2369.4; DB 6; Length 2371; Best Local Similarity 100.0%; Pred. No. 0; Matches 2370; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	ORIGIN /mol_type="unassigned DNA"

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98	940 AGAGGAGGACGTGGAGACCTGGAAAAATGGATAAAGGCGAGCACCGTCAGGAGG 	
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1879 1860	820 GGTGGAGACAGAGGTGGCTTCCGTGGTGGCCGGGCATGGACCGAGGTGGCTTTC 	
00 00	760 GGAGGAAGAGGTGGCCTCATGGATCGTGGTGGTCCCGGTGGAATGTTCAGAGGTGC 	
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1639 1620	GGAAACGTCCAGCACCGAGCTGGAGACTGGCAGTGTCCCAATCCGGGTTGTGGAAAAC 	
1579 1560	520 GATAGAGGAGGCTICCCTCCAAGAGGACCCCCGGGGTICCCGAGGGAACCCCTCIGGA 	
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1339 1320	280 GCCACAGTGTCCTATGAAGACCCACCCACTGCCAAGGCTGCCGTGGAATGGTTTGA 	
1279 1260	220 ACTGGGCAACCCATGATCCACATCTACCTGGACAAGGAAACAGGAAAGCCCCAAAGC 	
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JOURNAL , REMARK COMMENT	TITLE JOURNAL PUBMED REFERENCE AUTHORS TITLE	ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS	SULT 6 011048 CUS	N N 1	D Q D	Qy 21 Db 21 Qy 22	Qy 21 Db 21
Submitted (25-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgapbs-r@mail.nih.gov Tissue Procurement: Lou Staudt cDNA Library Preparation: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Preparation: Life Technologies Inc. cDNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center Center code: BCM-HGSC	Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaby, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevbhenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Sanchez, A., Whiting, M., Madan, J.W., Green, E.D., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Shewthenko, Y., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences 1 to 2364) ED 1247932 CE Chases I to 2364) Strausberg, R. Birect Submission	BC011048 BC011048.1 GI:15029674 MGC. MGC. MGC. Homo sapiens (human) Homo sapiens (bordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Craniata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Memmalia; Memmalia; Memmalia; Euteleostomi; Eukaryota; Memmalia; Memmali	BC011048 BC011048 BC011048 BC011048 BC011048 BC011048 BC011048 BC011048 BC011048 BC011048	60 CAATGTTTAATAAAAAAAAAAAAAAAA 2390	2221 TTTĀĀCĀĀTGGĞĀĀCCCCTTGTĞĀGCĀTĞCTCĀĞTĀTCATTGTĞGĀGĀĀCCĀAGAGGGCC 2280 2300 TCTTĀACĀTGAACAATGTTCATGGTTGTGATGTTTTTTTTTT	2180 TTAAATGGTAGTGTGCGGAGTTTTTTTTTTTTCTTCCTTC	120 GATTATTCCTTGTCTGTACTTTAGTATTTTTTCACCATTTGTGAAGAACATTAAAACAAG 2179

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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4885224.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged;
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
                                        TCCAACTGCCCCCAGGCATACAGCCAGCCTGTCCAGGGGTATGGCACTGGTGCTTATGA
    TACCACCACTGCTACAGTCACCACCACCCAGGCCTCCTATGCAGCTCAGTCTGCATATGG
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/t18sue_type="Lymph, lymphoma"
/clone_Tib="NIH_MGC_85"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                 Submitted (24-MAY-2004) Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: c22g@sanger.ac.uk Manuscript Sanger Institute name: pGEM.EWSR1 Homo sapiens cDNA sequence. This sequence was generated as part of The Wellcome Trust Sanger Institute program to isolate cDNA clones representing the full length open reading frame of well annotated protein coding genes on human chromosome 22. For more information see http://www.sanger.ac.uk/HGP/Chr22/.
                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2189)

Collins, J.E., Wright, C.L., Edwards, C.A., Davis, M.P., Grinham, J.A., Cole, C.G., Goward, M.E., Aguado, B., Mallya, M., Mokrab, Y., Huckle, E.J., Beare, D.M. and Dunham, I.

Direct Submission
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                                                                                 1. .\overline{2}189
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                                                               gene="EWSR1"
                                                                                            clone="pGEM.EWSR1"
'lab_host="JM109"
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19 frame
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2047 2094 1987

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Query Match
Best Local Similarity
Matches 2189; Conserv
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                                                                                                       GGACGTTGAGAGAACGAGGAAGGAAGAAAATGGCGTCCACGGATTACAGTACCTAT
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PGGMRGGRGGGHGKMDKGEHRQERNDRFY"
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                                                                                                                 GGCTTCCTCCCGCCACCCTTTCCGCCCCCCGGGTGGTGATCGTGGCAGAGGTGGCCCTGGT
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buctow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Willalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Glbbs, R.A.,

Fahey, J., Helton, B., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J. W., Green, B.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Schmerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

P. 1247932
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USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
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Homo sapiens Ewing sarcoma breakpoint region 1, transcript v
EWS, mRNA (cDNA clone MGC:5432 IMAGE:3449145), complete cds.
BC004817
BC004817.1 GI:13435962
                                                                                                                                                                                                                                                           Submitted (21-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                     Direct Submission
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121 145 61

GCATATGGGCAACAAGCTATGGAACCTATGGACAGCCCACTGATGTCAGCTATACCCA

GGCATATGGGCAACAAAGCTATGGAACCTATGGACAGCCCACTGATGTCAGCTATACCCA

204

144

60

120

85 GCAGCAGGGCTACAGTGCTTACACCGCCCAGCCCACTCAAGGATATGCACAGACCACCCA

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GCAGCAGGGCTACAGTGCTTACACCGCCCAGCCCACTCAAGGATATGCACAGACCACCCA

25 ш

Conservative

0

90.6%;

Score 2165; Di ; Pred. No. 0; 0; Mismatches

DB 9 0

Length 2182; Indels

0

Gaps

0

GGCTCAGACCACTGCAACCTATGGGCAGACCGCCTATGCAACTTCTTATGGACAGCCTCC GGCTCAGACCACTGCAACCTATGGGCAGACCGCCTATGCAACTTCTTATGGACAGCCTCC

300 324 240 264 180

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FEATURES
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This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs; R.A.
                                               PSGGGNVQHRAGDWQCPNPGCGNQNFAWRTECNQCKAPKPEGFLPPPFPPPGGDRGRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          choriocarcinoma"
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1165 AGATGATCTGGCAGACTTCTTTAAGCAGTGTGGGGTTGTTAAGATGAACAAGAGAAACTGG 1224	325 OACTGGTGCTTATGATACCACCACTGCTACAGTCACCACCCAGGCCTCCTATGCAGC 336
RESULT 10 BC072442 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS	D Q D Q D Q D D D D D D D D D D D D D D
BC072442 BC072442 Homo sapiens Ewing sarcoma breakpoint region 1, transcript variant EWS, mRNA (cDNA clone MGC:87992 IMAGE:6047805), complete cds. BC072442 BC072442. GI:48734726 Homo sapiens (human) Homo sapiens Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2164) Strausberg,R.L., Feingold, E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,	

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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Mational Institutes of Health Intramural
Sequencing Center (NISC),
Gatthersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
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Maduro,Q.L., Masiello,C., Maskeri,B., Mastrins,D.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Tand a. Zhang I. H. and Green, E. M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 174 Row: g Column: 18
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4885224. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Life Technologies.
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       host-"DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              melanoma."
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ORIGIN

Query Match Best Local Similarity

89.4%;

Score 2136; Pred. No. 0;

DB 9;

Length

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RESULT 11	2098 CTTTAGTATTTTTCACCATTTGTGAAGAAACATTAAAACAAGTTAAATGGTA 2149	2138 CTTTAGTATTTTTCACCATTTGTGAAGAAACATTAAAACAAGTTAAATGGTA 2189	2038 AAATTTATAATTCCATATTTATAATGTTGGCCACAACATTATGATTATTCCTTGTCTGTA 2097	2078 AAATTTATAATTCCATATTTATAATGTTGGCCACAACATTATGATTATTCCTTGTCTGTA 2137	1978 CAGAGACCCCGCAGAGCTGCATTGACTACCAGATTTATTT	2018 CAGAGACCCCGCAGAGCTGCATTGACTACCAGATTTATTT	1918 CCTGGAAAAATGGATAAAGGCGAGCACCGTCAGGAGCGCAGAGATCGGCCCTACTAGATG 1977	1958 CCTGGAAAAATGGATAAAGGCGAGCACCGTCAGGAGCGCCAGAGATCGGCCCTACTAGATG 2017

REFERENCE AUTHORS ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM AK056309 LOCUS DEFINITION Homo sapiens cDNA FLJ31747 fis, to RNA-BINDING PROTEIN EWS. AKO56309.1 GI:16551673
oligo capping; fis (full insert sequence)
Homo sapiens (human)
Homo sapiens Ota, T., Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Suzuki,Y., Nishikawa, T., Otsuki, T., Sugiyama, T., mRNA linear clone NT2RI2007377, Euteleostomi; Homo. PRI 30-JAN-2004 highly similar

TITLE Wakamatsu, A., Hayashi, K., Satto, H., Nagai, K., Kimura, K., Wakita, H., Shibahara, T., Tanaka, T., Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahari, K., Murakahi, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M., Shizatori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Shizatori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Shizatori, A., Sudo, H., Kanda, K., Yokoi, T., Furuya, T., Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T., Kikkawa, E., Omura, Y., Abe, K., Kamihara, K., Katsuta, M., Watanabe, M., Murakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M., Murakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M., Murakawa, S., Cohiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T., Sasaki, N., Aotsuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T., Sasaki, N., Aotsuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T., Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, T., Goto, Y., Shimtzu, F., Wakebe, H., Hishigaki, H., Watanabe, T., Sugiyama, A., Takura, S., Fukuzuni, Y., Fujimori, Y., Komatama, M., Tagaki, K., Hirao, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N., Nagase, T., Namira, Y., Ohamoto, S., Okitani, R., Kawakami, T., Nagase, T., Namira, Y., Takahashi, Y., Nakagawa, K., Pujii, Y., Satoh, T., Shigeta, K., Senba, T., Matsumura, K., Nakagawa, T., Nakagawa, K., Okumura, K., Nakagawa, T., Nakagawa, K., Okumura, K., Nakaguwa, Y., Wamashita, R., Nakaguno, S., Satoh, T., Nakaguno, S., Satoh, T., Andaha, K., Pujii, Y., Satoh, T., Nakagawa, T., Nakagawa, K., Okumura, K., Nakaguwa, Y., Wamashita, R., Nakaguno, S., Satoh, T., Anda Sugano, S., Satoh, T., Nakaguno, S., Nakagawa, K., Satoh, T., Nakaguno, S., Nakagawa, K., Satoh, T., Nakaguno, S., Nakagawa, K., Satoh, T., Nakaguno, S., Nakaguno, S., Satoh, T., Nakaguno, S., Nakaguno, S., Satoh, T., Nakaguno, S., Nakaguno, S., Nakagun Genet. 36 (1), 40-45 (2004) Makita, H.,

Ishibashi,T., Kanehori,K., Yosida,M., Watanabe,S., Ishida,S., Ono,Y., Hotuta,T., Hiraoka,S., Murakawa,K., Takiguchi,S., Kusano,J., Watanabe,M., Fujimori,K., Tanai,H., Ishida,M., Yamashita,H., Chiba,Y., Sugiyama,T., Irie,R., Oteuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y., Wakamatsu,A., Ishii,S., Yamamoto,J., Hono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Watsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'-& 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: RAB and
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Isogai, T., Otsuki, T. and Sugiyama, T.
Direct Submission
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/codon_start=1
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/db_xref="taxon:9606"
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Eukaryota; Metazoa; (Chordata; Cat
Mammalia; Eutheria; Primates; Cat
1 (bases 1 to 193559)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 10
2 (bases 1 to 193559)
DOB Joint Genome Institute
Direct Submission
                                                                                                                                                   AC137500 PAA linear HT HOMO SEQUENCE, 2 unordered pieces.
AC137500 AC137500 AC137500.1 GI:25139894 HTGS PHASEL; HTGS DRAFT; HTGS_ACTIVEFIN.
HOMO Sepiens (human)
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                                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Consensus quality: 192718 bases at least Q40
Consensus quality: 192915 bases at least Q30
Consensus quality: 193071 bases at least Q30
Consensus quality: 193071 bases at least Q20
Estimated insert size: 160000; agarose-fp estimation
Bstimated insert size: 193459; sum-of-contigs estimation
Quality coverage: 10.21 in Q20 bases; agarose-fp estimation
Quality coverage: 10.21 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
                                                                                                                                      30744
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Center clone name: RPCI-11_343G17
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Center: Joint Genome Institute
Center Code: JGI
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GGCAGCAGCCAGCCACTGCACCTACAAGACCGCAGGATGGAAACAAGCCCACTGAGA 485
                                           CCCAGGCCTCCTATGCAGCTCAATCTGCATATGGCACTCAGCCTGCTTATCCAGCTTATG
                                                                     CCCAGGCCTCCTATGCAGCTCAGTCTGCATATGGCACTCAGCCTGCTTATCCAGCCTATG
                                                                                                                                 AGCCTGTCCAGGGGTATGGCACTGGTGCTTATGATACCACCACTGCTACAGTCACCACCA
                                                                                                                                                             AGCCTGTCCAGGGGTATGGCACTGGTGCTTATGATACCACCACTGCTACAGTCACCACCA
                                                                                                                                                                                                                                CTTCTTATGGACAGCCTCCCACTGGTTATACTACTCCAACTGCCCCCCAGGCATACAGCC
                                                                                                                                                                                                                                                      CTTCTTATGGACAGCCTCCCACTGGTTATACTACTCCAACTGCCCCCCAGGCATACAGCC
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/clone_lib="RPCI human BAC
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Pred. No. 0;
0; Mismatches
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	1506 GAGGCCGTGGAGGAGATAGAGGAGGCTTCCCTCCAAGAGGACCCCCGGGGTTCCCCAAGGGA 1565
<u>.</u>	1446 CACCACTCCGTGGAGGTCCAGGAGGCCCAGGAGGTCCTGGGGGGACCCATGGGTCGCATGG 1505
REFE	1386 AGCCTCCAATGAACAGTATGCGGGGTGGTCTGCCACCCCGTGAGGGCAGAGGCATGCCAC 1445
REFE AU TI	1326 AATGGTTTGATGGGAAAGATTTTCAAGGGAGCAAACTTAAAGTCTCCCTTGCTCGGAAGA 1385
SOUR	1266 AGCCCAAAGGCGATGCCACAGTGTCCTATGAAGACCCACCGACTGCCAAGGCTGCCGTGG 1325
ACCE	1206 AGATGAACAAGAGAACTGGGCAACCCATGATCCACATCTACCTGGACAAGGAAACAGGAA 1265
RESU ACO1 LOCU	1146 TAAATGACAGTGTGACTCTAGATGATCTGGCAGACTTCTTTAAGCAGTGTGGGGTTGTTA 1205
Db 43	1086 TAGGCCCACCTGTAGATCCAGATGAAGACTCTGACAACAGTGCAATTTATGTACAAGGAT 1145
5 B 8	1026 GAGAGCGAGGTGGCTTCAATAAGCCTGGTGGACCCATGGATGAAGGACCAGATCTTGATC 1085
) p 9	966 ATCGTGGAGGCATGAGCAGAGGTGGGCGGGGAGGAGGAGGAGGCGCTGTGGAATGGGCAGCGCTG 1025
) B 4	906 CAGGAGAGAACCGGAGCATGAGTGGCCCTGATAACCGGGGCAGGGGAAGAGGGGGATTTG 965
5 B &	846 GACAGGACCACCCCAGTAGCATGGGTGTTTATGGGCAGGAGTCTGGAGGATTTTCCGGAC 905
2 pg 4	786 GCCAAGCTCCAAGTCAATATAGCCAACAGAGCAGCAGCAGCTACGGGCAGCAGAGTTCATTCC 845
) b &	726 AACAAAGCAGCTATGGGCAGCAGCCTCCCACTAGTTACCCACCC
) b 4	666 ACTCTCAGCAGAACACCTATGGGCAACCGAGCAGCTATGGACAGCAGAGTAGCTATGGTC 725
S & &	606 CATCCTACCCTCCTACCAGCTATTCCTCTACACAGCCGACTAGTTATGATCAGAGCAGTT 665
) B &	546 GTAACTACAGTTATCCCCAAGTACCTGGGAGCTACCCCATGCAGCCAGTCACTGCACCTC 605
p 9	486 CTAGTCAACCTCAATCTAGCACAGGGGGGTTACAACCAGCCCAGCCTAGGATATGGACAGA 545

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AACATTAAAACAAGTTAAATGGTA 2189 AACATTAAAACAAGTTAAATGGTA 28863	GGCCACAACATTATGATTATTCCTTGTGTGTGTACTTTAGTATTTTTCACCATTTGTGAAGA 2165 	CCAGATTIAITTITAAACCAGAAAATGTITTAAAITTAIAATTCCATATTIATAATGTT 2105 	GTCAGGAGCGCAGAGATCGGCCCTACTAGATGCAGAGACCCCGCAGAGCTGCATTGACTA 2045	AGATGGGAAGAAGAAGAAGAAGGACGTGGAAGAAAATGGATAAAGGCGAGCACC 1985 	GTGGCTTTGGTGGAGGAAGACGAGGTGGCCCTGGGGGGGCCCCTGGACCTTTGATGGAAC 1925 	TCAGAGGTGGCCGTGGTGGAGACAGAGGTGGCTTCCGTGGTGGCCGGGGCATGGACCGAG 1865	CTGGTGGCATGCGGGAAGAAGAGGTGGCCTCATGGATCGTGGTGGTGGTCCCGGTGGAATGT 1805	CTGAAGGCTTCCTCCGGCCACCCTTTCCGCCCCCGGGTGGTGATCGTGGCAGAGGTGGCC 1745	GTTGTGGAAACCAGAACTTCGCCTGGAGAACAGAGTGCAACCAGTGTAAGGCCCCCAAAGC 1685 	ACCCCTCTGGAGGAAAACGTCCAGCACCGAGCTGGAGACTGGCAGTGTCCCAATCCGG 1625	GAGGCCGTGGAGGAGATAGAGGAGGCCTCCCTCCAAGAGGACCCCCAGGGTTCCCCGAGGGA 29485

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JOURNAL
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Best Local Similarity
Matches 2103; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassillev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Zimmer, A.
6 GAGACGGACGTTGAGAGAAGGAGGAGGAGGAGAAAATGGCGTCCACGGATTACAGTA
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----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
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Center clone name: 20_G3
Sequencing vector: M13, M77815; 100% of reads
Sequencing vector: M13, M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 150190 bases at least Q40
Consensus quality: 153191 bases at least Q20
Consensus quality: 153404 bases at least Q20
Insert size: 155615; sum-of-contigs
Quality coverage: 5.1 in Q20 bases; sum-of-contigs
Quality coverage: 5.2 in Q20 bases; sum-of-contigs
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Contact: sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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6153
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23234. ... 155815
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6153. .23133
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/db_xref="taxon:9606"
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                                                                                                            85.1%;
96.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _lib≐"RPCI-11 Human Male BAC"
                                                                                     0;
                                                                                                               Score 2033.6;
Pred. No. 0;
                                                                                        Mismatches
                                                                                                                                      DB 2;
                                                                                     79;
                                                                                        Indels
                                                                                                                                         Length 155815;
                                                                                   2; Gaps
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PRI 10-MAR-2002 ne 1, complete

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                                                                                AACATTAAAACAAGTTAAATGGTA 2189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGGTGGCATGTGGGGAGGAAGAGGTGGCCTCATGGATCATGGTGGTCCCGGTGGAATGT 12148
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; TT:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.Banger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at http://www.Banger.ac.uk/HGP/Chr1
RP11-9118 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
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Location/Qualifiers
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1. (bases 1 to 180718)
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for the note(s) - [] Tandem repeat [] Single clone
region [] Forced join [x] Other Add a comment here -
sequence from AC011221 and AC018774 sequenced by WIBR."
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short insert library derived from a single pUC clone.
Restriction digest data confirm the assembly."
complement (10216..102124)
/note="767 bases of IS1 transposon (X52534) removed here.
This sequence represents the duplicated flanking sequence
of the IS1."
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Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,

Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (03-OCT-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Sep 4, 2000 this sequence version replaced gi:7341864. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
* arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence
                                                           * NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia, Eutheria, Primates, Cat
1 (bases 1 to 182501)
Birren, B., Linton, L., Nusbaum, C.
Homo sapiens, clone RP11-9L18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC011221 182501 |
Homo sapiens clone RP11-9L18,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                        Sequencing vector: M13; M77815; 100% of reads Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 175883 bases at least Q40 Consensus quality: 179186 bases at least Q30 Consensus quality: 180361 bases at least Q20 Insert size: 182000; agarose-fp Insert size: 181001; sum-of-contigs
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Center clone name: 9_L_18
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sum-of-contigs
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                        6 GAGACGGACGTTGAGAGAACGAGGAGGAAGGAGAGAAAATGGCGTCCACGGATTACAGTA
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|mol_type="genomic DNA"
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g of 1404 bp
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REFERENCE AUTHORS

JOURNAL

Jnpublished

COMMENT

Center code: WIBR

JOURNAL

Wyman,D., Ye,W.J., Direct Submission

REFERENCE AUTHORS TITLE

SOURCE ORGANISM

Homo sapiens

ACCESSION VERSION

KEYWORDS

RESULT 15 AC011221 LOCUS

DEFINITION

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GAGAGCAAGTTGGCTTCAATAAGCCTGGTGGACCCATGGATGAAGGACCAAGTTTGATC 57523 TAGGCCCACCTGTAGATCCAGATGAAGACTCTGACAACAGTTGCAATTTATGTACAAGGAT 1145	ATCGTGGAGGCATGAGCAGAGGTGGGCGGGGAGGAGGACGCGGTGGAATGGGCAGCGCTG 1025			GCCAAGCTCCAAGTCAATATAGCCAACAGAGCAGCAGCAGCAGCAGCAGCAGAGTTCATTCC 845	AACAAAGCAGCTATGGGCAGCAGCCTCCCACTAGTTACCCACCC	ACTCTCAGCAGAACACCTATGGGCAACCGAGCAGCTATGGACAGCAGAGTAGCTATGGTC 725	CATCCTACCTCCTACCAGCTATTCCTCTACACAGCCGACTAGTTATGATCAGAGCAGTT 665	GTAACTACAGTTATCCCCAGGTACCTGGGAGCTACCCCATGCAGCCAGTCACTGCACCTC 605	CTAGTCAACCTCAATCTAGCACAGGGGGTTACAACCAGCCCTAGGCTAGGATATGGACAGA 545 CTAGTCAACCTCAATCTAGCACAGGGGGTTACAACCAGCCCTAGGATATGGACAGA 56983	GGCAGCAGCAGCACCTGCACCTACAAGACCGCAGGATGGAAACAAGCCCACTGAGA 485	CCCAGGCCTCCTATGCAGCTCAGTCTGCATATGGCACTCAGCCTGCTTATCCAGCCTATG 425	AGCCTGTCCAGGGGTATGGCACTGGTGCTTATGATACCACCACTGCTACAGTCACCACCA 365	CTTCTTATGGACAGCCTCCCACTGGTTATACTACTCCAACTGCCCCCAGGCATACAGCC 305	CTGATGTCAGCTATACCCAGGCTCAGACCACTGCAACCTATGGGCAGACCGCCTATGCAA 245	GATATGCACAGACCACCCAGGCATATGGGCAACAAAGCTATGGAACCTATGGACAGCCCA 185	CCTATAGCCAAGCTGCAGCGCAGGGCTACAGTGCTTACAACACCCAGCCCAAGCTCAAG 56563
	2016 CCAGALIA IIII IIII IIIIIIIIIIIIIIIIIIIIIII	1986 GTCAG	GAGGAAGAAGACGACGACCTGGACCTGGAAAATGGATAAAGGCGAGCACC 	1866 GTGGCTTTGGTGGAAGAACGAGGTGGCCCTGGGGGGGCCCCCTGGACCTTTGATGGAAC		58184 CTGGTGGCATGTGGGAGAAGAGGTGGCCTCATGGATCATGGTGGTCCCCGGTGGAATGT	1746 CTGANGGETTECTECCGCCACCETTTCCCCCCGGGTGGTGGTCGTCGGTGGAATGT	1626 GTIGH 58064 GTIGH	1506 ACCUCIL USANGSINGAMANG I CONCUNCICUS GENERAL ISOCIATION (CONTINUE CONTINUE CONT	1506 GAGGC 57944 GAGGC	1446 CACCA 57884 CACCA	AGCCTCCAATGAACAGTATGCGGGGTGGTATGCCACCCCGTGAGGGCAGAGGGATGCCAC	1326 AAIGGIIIGA GOGANAGAIIIICANOOSONOOMAACIIANOOICICCCIIGGICOGAAGA [1266 AGCCC 57704 AGCCC	1206 AGATGAACAAGAACHAGGACCAATGATCAACATCTACCTGGACAACGAAACAAGAACAAGAACTGAGCAAGAACAAGAACAAGAACAAGAACAAGAAACAAAGAAACAAAGAAACAAGAAACAAGAAACAAGAAACAAGAAACAAAGAAAAAA	57584 TANATGACAATGTGACTCTAGATGATCTGGTAGACTTCTTTAAGCAGTGTGGGGTTGTTA

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          WPI; 2002-435328/46
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                                                                                                                                                                                        Homo sapiens
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                                  Beazer-Barclay Y,
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                                                                                                                                                                                                                                                                                                    granulocytic cell; DNA chip; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                           INC.
                                     Weissman
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                                  Yamaga S,
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Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and drug toxicity.

Claim 1; SEQ ID NO 1199; 114pp; English.

CC (GCA), by detecting the level of expression of gene(s) (GS) identified by CC DNA chip analysis as given in the specification, and comparing the CC expression level to an expression level in an unactivated GC, where CC differential expression of Gs is indicative of GCA. Also included are CC modulating (M2) GA by contacting GC with an agent that alters the CC expression of at least one gene in Gs; (2) screening (M3) for an agent Ctissue, an allergic response in a subject, exposure of a subject to a CC pathogen or sterile inflammatory disease using the gene expression of the gene in a subject, exposure of a subject to a CC pathogen or sterile inflammatory disease, by detecting the level of CC expression in a sample of the tissue of gene(s) from Gs, where the level of CC expression in a subject of the tissue of inflammation; (4) treating CC (M5) an inflammation (especially chronic) in a CC inflammatory disease, by contacting a tissue having inflammation with an CC inflammatory disease, by contacting a tissue having inflammation with an CC inflammatory disease, by contacting a tissue having inflammation with an CC inflammatory in a tissue, an allergic response in a subject to a pathogen or sterile for screening an agent capable of modulating GCA preferably in an CC inflammation in a tissue; M1 is useful for modulating GA; M3 is useful for screening an agent capable of modulating GCA preferably in an CC exposure of a subject to a pathogen or sterile inflammation in a tissue, an allergic response in a subject, capable of modulating GCA preferably in an CC exposure of a subject to a pathogen or sterile inflammation of gene(s) from Gs in the tissue. M1 is useful for detecting an inflammation of gene(s) from Gs in the tissue. M2 is useful for terminating GCA preferably in an inflammation of gene (s) from Gs in the tissue. M2 is useful for terminating GCA preferably in an inflammation of gene (s) from Gs in the tissue (s.g. genetatory distaces syndrome, inflammatory bowel disease, country of genetal genetal genetal gen electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences The invention relates to detecting (M1) granulocyte (GC) activation thrombosis, M3 is useful level M an ġ à

Sequence 2390 BP; 645 A; 589 C; 668 G; 488 T; 0 U; 0 Other;

Query Match Best Local Similarity Matches 2389; Conserv Conservative 99.9%; Score 2388.4; Pred. No. 0; Mismatches В ŗ 6 Indels Length 2390; 0; Gaps 0;

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`	1 AGAGGGAGACGGACGTTGAGAGAAACGAGGAGGAAGGAGAAAAATGGCGTCCACGGATTA 60	_
J	1 AGAGGGAGACGTTGAGAGAAACGAGGAGGAGAGAGAAAATGGCGTCCACGGATTA 60	-
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J	61 CAGTACCTATAGCCAAGCTGCAGCGCGAGGGCTACAGTGCTTACACCGCCCAGCCCAC 120	Ö
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•	181 GCCCACTGATGTCAGCTATACCCAGGCTCAGACCACTGCAACCTATGGGCAGACCGCCTA 240	0
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	241 TGCAACTTCTTATGGACAGCCTCCCACTGGTTATACTACTCCCAACTGCCCCCCAGGCATA 300	Ō
Ū	241 TGCAACTTCTTATGGACAGCCTCCCACTGGTTATACTACTCCAACTGCCCCCCAGGCATA 300	0
	301 CAGCCAGCCTGTCCAGGGGTATGGCACTGGTGCTTATGATACCACCACTGCTACAGTCAC 360	0
Ü	301 CAGCCAGCCTGTCCAGGGGTATGGCACTGGTGCTTATGATACCACCACTGCTACAGTCAC 360	0
	361 CACCACCCAGGCCTCCTATGCAGCTCAGTCTGCATATGGCACTCAGCCTGCTTATCCAGC 420	0

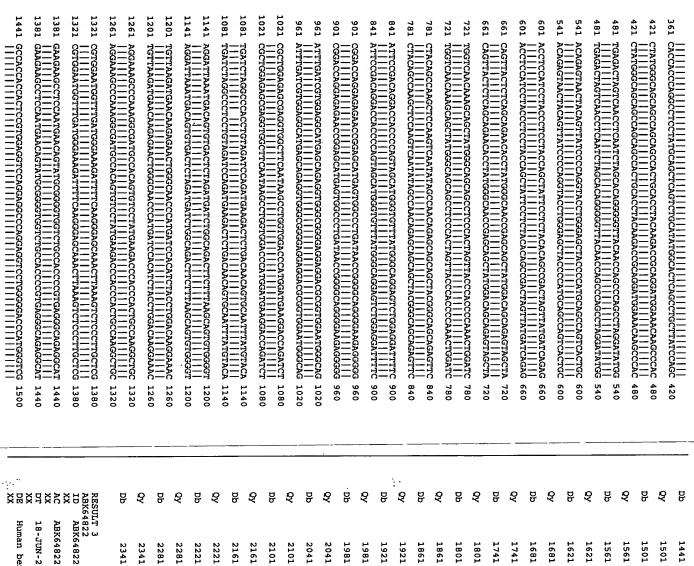
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standard; 2390 ВP

18-JUN-2002 (first entry)

Human benign prostatic hyperplasia gene

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                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a method of diagnosing (I) the onset or CC progression of benign prostatic hyperplasia (BPH), or screening (II) for CC or identifying an agent that modulates the onset or progression of BPH. CC The method is based on changes in gene expression in BPH tissue isolated (CC from patients exhibiting different clinical states of prostate (CC from patients exhibiting different agency in the subject that are differentially regulated compared to normal prostate certing the expression levels of one or more genes in prostate cells (II) comprises (CC from the subject that are differentially regulated compared to normal (CC prostate cells. (II) comprises preparing a first gene expression profile of BPH cells or BPH-like cell population, exposing the cells to the cells, preparing a second gene expression profile of the agent exposed (CC agent, preparing a second gene expression profiles. (I) is useful for diagnosing the first and second gene expression profiles. (I) is useful for identifying an agent that modulates the onset or progression of BPH. (CC in methods are useful to present information identifying the expression (CC expression of gene in the database, and displaying the expression levels of at least one gene in the database, and displaying the expression levels (CC expression of gene in the database, and displaying the expression levels (CC prostate cancer. ABK64106-ABK64860 represent human benign prostatic very constatic concerts of the invention (CC prostate cancer. ABK64106-ABK64860 represent human benign prostatic very constatic constant in the invention (CC prostate cancer. ABK64106-ABK64860 represent human benign prostatic very constant cancer.
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Best Local Similarity
Matches 2389; Conserv
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Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic; metastatic liver tumour; cytostatic; expression profile; disease si disease progression; drug toxicity; drug efficacy; drug metabolism
                                                                                                                                                                                Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a patient, involves detecting the level of expression of two or more genes in a liver tissue sample.
                                                                                                                                                                                                                                                                                                                                                                                                           Gene #3772 used to diagnose liver cancer
                                                                                                                                                                                                                                                                              02-OCT-2000; 2000US-0237054P
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state;

The invention relates to a novel method for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumour in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, involving detecting the level of expression of two or more genes represented in ABN93503-ABN97455 in a tissue sample. The method of the invention has hepatotropic, and cytostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, drug toxicity, drug efficacy and drug metabolism. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

SEQ ID NO 3772; 298pp; English.

Sequence 2390 BP; 645 A; 589 C; 668 G; 488 T; 0 U; 0 Other;

Query Match Best Local Similarity Matches 2389; Conserv

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Score 2388.4; ; Pred. No. 0; 0; Mismatches

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                                                                                                                                                             polypeptides; expression vectors and host cells comprising a TAT nucleic acid; an antibody specific for a TAT polypeptide; fusion proteins comprising a TAT polypeptide; fusion proteins comprising a TAT polypeptide; fusion proteins comprising a TAT polypeptide; fusion for the treatment or diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder cancer, pancreatic cancer, cervical cancer, cancers of the central nervous system, melanoma and leukaemia. TAT nucleic acids may further be used as hybridisation probes, in chromosome and gene mapping, in cromosome identification and in gene therapy. The present sequence
                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumour-associated antigenic target; TAT; human; overexpression; citumour; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoma; leukaemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping;
                                                                                                                                                                                                                                                                                                                                          The invention relates to human tumour-associated antigenic target (TAT) polypeptides, and their related nucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide sequences at least 80% identical to the TAT nucleic acids and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or
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                                       The probes 22RR3 and 22RR12 were used to screen a human foetal brain library (Stratagene cat.# 936206). The clone BFLAC5 was identified an sequenced. It represents the entire coding region and 3'-UTR of the gene. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                              New nucleic acid of EWS gene and its hybrid(s) - contg. gene sequence involved in chromosomal trans-location, also derived mRNA, probes, fusion proteins etc., for diagnosis and treatment of Ewing sarcoma and melanoma.
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	2120 GATTAITCCTTGTCTGTACTITIAGTATITTTCACCATTTGTGAAGAACAITAAAACAAG 2179		2000 GATCGGCCCTACTAGATGCAGAGACCCCGCAGAGCTGCATTGACTACCAGATTTATTT	1940 AGAGGAGGACGTGGAGGACCTGGAAAAATGGATAAAGGCGAGCACCGTCAGGAGCGCAGA 1999 	1880 GGAAGACGAGGTGGCCCTGGGGGGCCCCCTGGACCTTTGATGGAACAGATGGGAGGAAGA 1939 	1820 GGTGGAGACAGAGGTGGCTTCCGTGGTGGCCGGGGCATGGACCGAGGTGGCTTTGGTGGA 1879 	1760 GGAGGAAGAGGTGGCCTCATGGATCGTGGTGGTCCCGGTGGAATGTTCAGAGGTGGCCGT 1819	1700 CCGCCACCCTTTCCGCCCCCGGGTGGTGATCGTGGCAGAGGTGGCCCTGGTGGCATGCGG 1759	1640 AACTTCGCCTGGAGAACAGAGTGCAACCAGTGTAAGGCCCCAAAGCCTGAAGGCTTCCTC 1699 	1580 GGAAACGTCCAGCACCGAGCTGGAGACTGGCAGTGTCCCAATCCGGGTTGTGGAAACCAG 1639 	1520 GATAGAGGAGGCTTCCCTCCAAGAGGACCCCGGGGTTCCCGAGGGAACCCCTCTGGAGGA 1579	1460 GGTCCAGGAGGCCCAGGAGGTCCTGGGGGACCCATGGGTCGCATGGGAGGCCGTGGAGGA 1519	1400 AGTATGCGGGGTGGTCTGCCACCCCGTGAGGGCAGAGGCATGCCACCACCACTCCGTGGA 1459	1340 AAAGATTTTCAAGGGAGCAAACTTAAAGTCTCCCTTGCTCGGAAGAAGCCTCCAATGAAC 1399 		1220 ACTGGGCAACCCATGATCCACATCTACCTGGACAAGGAAACAGGAAAGCCCAAAGGCGAT 1279 	1160 ACTCTAGATGATCTGGCAGACTTCTTTAAGCAGTGTGGGGGTTGTTAAGATGAACAAGAGA 1219

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potentiating effect of the above protein; (13) a method of therapeutically treating a mammal having a cancerous tumour comprising	the growth of the cell is at least in part dependent upon a growth	the composition of matter contained within the container; (12) methods of	with a carrier; (11) an article of manufacture comprising a container and	composition of matter comprising the above (chimeric) polypeptide,	binding organic molecule that binds to the above polypeptide; (10) a	for producing the antibody; (8) an isolated oligopeptide that binds to	an isolated antibody that binds to the above polypeptide; (7) a process	comprising the above polypeptide fused to a heterologous polypeptide:	length coding region of the above nucleotide sequences; or (c) a sequence	nucleotide sequences; (b) an amino acid sequence encoded by any of the above	a process for producing a polypeptide; (4) an isolated polypeptide	(C). Also described: (1) an expression vector comprising the above nucleic acid; (2) a host cell comprising the above expression vector: (3)	sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-	<pre>sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of (a); (c) the complement of (a) or (b); (d) a sequence that has 80*</pre>	C The present invention describes an isolated tumour-associated antigenic target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide	Claim 1; SEQ ID NO 2904; 5504pp; English.	New nucleic acid molecule and encoded polypeptide, for diagnosing, preventing or treating cell proliferative disorders such as cancer.	WPI; 2004-534300/51.	Wu TD, Zhou Y;	(ZHOU/) ZHOU Y.	(GETH) GENENTECH INC.	18-OCT-2002; 2002US-0418988P.	15-OCT-2003; 2003WO-US029126.	22-JUL-2004.	WO2004060270-A2.	Homo sapiens.	human; tumour-associated antigenic target; TAT; cytostatic; gene therapy; cancer; cell proliferative disorder; gene; ss.	Human tumour-associated antigenic target (TAT) cDNA sequence #2904.	07-OCT-2004 (first entry)	ADQ86032;	RESULT 7 ADQ86032 ID ADQ86032 standard, cDNA, 2372 BP.	2341 CAAATGTTTAATAAAAAAAAAAAAAAAAAAAAAAAAAAA	2360 CAAATGTTTAATAAAAAAAAAAAAAAA 2390	2281 TCTTAACTGTAACAATGTTCATGGTTGTGATGTTTTTTTT	2221 TTTAACAATGGGAACCCCTTGTGAGCATGCTCAGTATCATTGTGGAGAACCAAGAGGGCC 2280

cells that express the above protein; (14) a method of determining the presence of a protein in a sample suspected of containing the protein described above; (15) methods of diagnosing the presence of a tumour in a mammal; (16) a method for treating or preventing a cell proliferative disorder associated with increased expression or activity of the above protein; and (17) a method of binding an antibody, oligopeptide or organic molecule to a cell that expresses the protein described above. The TAT sequences have cytostatic activities, and can be used in gene. therapy. The composition and methods are useful for diagnosing, preventing or treating cancer. The composition is also used for preparing a medicament for the therapeutic treatment or diagnostic detection of a cell proliferative disorder or cancer. The present sequence represents a human TAT CDNA sequence from the present invention.

Sequence 2372 BP; 628 A; 589 C; 668 G; 487 T; 0 U; 0 Other;

Query Match Best Local Simi Matches 2370;

Similarity

98.7%;

Score 2357.8; Pred. No. 0; 0; Mismatches

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Conservative

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Gaps

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AAS70647 standard; CDNA; 2388 ₽P

13-FEB-2002 (first entry)

DNA encoding novel human diagnostic protein #6451.

Human; chromosome food supplement; m ne mapping; medical im j; gene mapping; gene therapy; imaging; diagnostic; genetic disorder;

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Homo sapiens

WO200175067-A2

30-MAR-2001; 2001WO-US008631

31-MAR-2000; 2000US-00540217. 23-AUG-2000; 2000US-00649167.

(HYSE-) HYSEQ INC.

Drmanac 평, Liu C, Tang ĭ

WPI; 2001-639362/73. P-PSDB; ABG06460.

RESULT 1
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XX Huma
DE DNA FOOC
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XX Ho New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.

Claim 1; SEQ Ħ ö 6451; 103pp; English

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CR sequences. (I) is useful as hybridisation probes, polymerase chain
CR reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CR and in recombinant production of (II). The polynucleotides are also used
CR in diagnostics as expressed sequence tags for identifying expressed
CR in diagnostics as expressed sequence tags for identifying expressed
CR cactivity of (II) or to treat disease states involving (II). (II) is
CR useful for generating antibodies against it, detecting or quantitating a
CR polypeptide in tissue, as molecular weight markers and as a food
CR supplement. (II) and its binding partners are useful in medical imaging
CR involving aberrant protein expression or biological activity. The
CR diagnostics, forensics, gene mapping, identification of mutations
CR diagnostics, forensics, gene mapping, identification of mutations
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CR and to produce other types of data and products dependent on DNA and
CR and to produce other types of data and products dependent on DNA and
CR amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CR patent did not appear in the printed specification, but was obtained in
CR electronic format directly from WIPO at
CR ftp.wipo.int/pub/published_pct_sequences
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                GGCCCTGGTGGCATGCGGGGAAGAAGATGGTCGTCATGGATCGTGGTGGTCCCGGTGGA 1801
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ঠ 밁 S 밁 Ş 밁 र् 뭐 Ş 밁

WPI; 2002-010900/01

New polynucleotides encoding secreted asthma, HIV and Crohn's disease. proteins useful for treating e.g.

Page 291; 391pp; English

The present invention relates to the isolation of novel cDNA sequences CC which encode human secreted proteins. The cDNA sequences have been CC derived from a variety of human tissues. The invention also provides a CC method for producing proteins from these polynucleotide sequences. The CC proteins are useful for identifying compounds that modulate their CC compounds that modulate expression of the polynucleotide sequences (compounds that modulate expression of the polynucleotide sequences (concoding the secreted proteins. The sequences of the invention are useful CC for treating diseases such as hyperproliferative disorders (e.g. cancer), cmmune deficiency disorders (e.g. severe combined immunodeficiency (SCID)), autoimmune disorders (e.g. multiple sclerosis), blood disorders (e.g. thrombocytopaenia), inflammatory disorders (e.g. arthritis) and CC (screttious disorders (e.g. hepatitis). The polynucleotide sequences of the invention are also useful in gene therapy. AAS62214-AAS62838 CC represent the CDNA sequences of the invention that encode for novel human constraints. proteins

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Sequence 2273 BP; 477 A; 636 Ç 562 G; 598 T; 0 U; 0 Other;

В

6;

Indels Length 2273;

54;

Gaps

Query Match 91.2%; Best Local Similarity 97.3%;

Conservative

S 밁 á S 밁 S 밁 S 밁 Ś 밁 S 밁 S 밁 ঠ 밁 S 밁 밁 Matches 2259; 1728 1848 1968 2028 2088 2148 2208 2268 1668 1788 1908 162 642 582 522 462 402 342 282 222 102 42 CAACTGCCCCCAGGCATACAGCCAGCCTGTCCAGGGGTATGGCACTGGTGCTTATGATA CTTACACCGCCCAGCCCACTCAAGGATATGCACAGACCACCCAGGCATATGGGCAACAAA CGACTAGTTATGATCAGAGCAGTTACTCTCAGCAGAACACCTATGGGCAACCGAGCAGCT CGACTAGTTATGATCAGAGCAGTTACTCTCAGCAGAACACCTATGGGCAACCGAGCAGCT CCATGCAGCCAGTCACTGCACCTCCATCCTACCAGCTATTCCTCTACACAGC CCACCACTGCTACAGTCACCACCACCCAGGCCTCCTATGCAGCTCAGTCTGCATATGGCA CCTATGGGCAGACCGCCTATGCAACTTCTTATGGACAGCCTCCCACTGGTTATACTACTC GCTATGGAACCTATGGACAGCCCACTGATGTCAGCTATACCCAGGCTCAGACCACTGCAA GCTATGGAACCTATGGACAGCCCACTGATGTCAGCTATACCCAGGCTCAGACCACTGCAA CTTACACCGCCCAGCCCACTCAAGGATATGCACAGACCACCCAGGCATATGGGCAACAAA AAGGTGCGTCCACGGATTACAGTACCTATAGCCAAGCTGCAGCGCAGCAGGGCTACAGTG AAATGGCGTCCACGGATTACAGTACCTATAGCCAAGCTGCAGCGCCAGCAGGGCTACAGTG AGCCCAGCCTAGGATATGGACAGAGTAACTACAGTTATCCCCAGGTACCTGGGAGCTACC AGGATGGAAACAAGCCCACTGAGACTAGTCAACCTCAATCTAGCACAGGGGGTTACAACC CTCAGCCTGCTTATCCAGCCTATGGGCAGCAGCCAGCAGCCACCTGCACCTACAAGACCGC CCACCACTGCTACAGTCACCACCACCCAGGCCTCCTATGCAGCTCAGTCTGCATATGGCA CCTATGGGCAGACCGCCTATGCAACTTCTTATGGACAGCCTCCCACTGGTTATACTACTC 0; Score 2179.6; Pred. No. 0; 0; Mismatches 9; 581 1969 341 161 101 1609 1669 1729 1789 521 1849 461 1909 401 2089 2149 2209 641 2029 701 281 221

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RESULT 10
AAS62262/c
ID AAS6222
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XX AAS622
XX AAS622
XX AAS622
XX Human
KW Human
KW infect
KW infect
KW infect
XW inmuno
XX Inmuno
XX IO2001
XX HOGON
XX GEMY
XX GEMY
XX GEMY
XX GULUKO
XX WPI, 2
XX WPI, 2 AAS62262 AAS62262 standard; CDNA; 2176 ВP

cDNA sequence #49 encoding novel human secreted protein. 14-FEB-2002

(first

entry)

Human secreted protein; hyperproliferative disorder; autoimmune disorder; immune deficiency disorder; blood disorder; inflammatory disorder; infectious disorder; gene therapy; antimicrobial; hepatotropic; immunosuppressive; antirheumatic; ss.

WO200177291-A2

18-OCT-2001.

29-MAR-2001; 2001WO-US010485

06-APR-2000; 2000US-0195604P

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(GEMY) GENETICS INST INC

Wong GG, Clark HF, Gulukota K, Graham Graham Fechtel K, Agostino 3 Howes SH, 꼰

WPI; 2002-010900/01

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The present invention relates to the isolation of novel cDNA sequences which encode human secreted proteins. The cDNA sequences have been derived from a variety of human tissues. The invention also provides a method for producing proteins from these polynucleotide sequences. The proteins are useful for identifying compounds that modulate their cativity and production, and the cell is also useful for identifying compounds that modulate expression of the polynucleotide sequences compounds that modulate expression of the polynucleotide sequences cancoding the secreted proteins. The sequences of the invention are useful for treating diseases such as hyperproliferative disorders (e.g. cancer), immune deficiency disorders (e.g. severe combined immunodeficiency (SCID)), autoimmune disorders (e.g. multiple sclerosis), blood disorders (e.g. thrombocytopaenia), inflammatory disorders (e.g. arthritis) and infectious disorders (e.g. hepatitis). The polynucleotide sequences of the invention are also useful in gene therapy. AAS52214-AAS52838
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Matches 2154; Conserv
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The invention relates to human tumour-associated antigenic target (TAT) polypeptides, and their related nucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in
                                                                                                                          New tumor-associated antigenic target polypeptides and nucleic useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian
                                                                                                                                                                                                                                                                                                        02-OCT-2002; 2002US-0414971P
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                                                                                    CC mammals. The invention also relates to nucleic acid and polypeptide gequences at least 80% identical to the TAT nucleic acids and collected and polypeptides; expression vectors and host cells comprising a TAT nucleic acid, an antibody specific for a TAT polypeptide; a peptide or organic conformal composition and methods and compositions for the treatment or collectule which binds to a TAT polypeptide; fusion proteins comprising a CC TAT polypeptide; an antibody appear of the methods and compositions for the treatment or collectual cancer, antagonists, binding molecules and compositions are useful corrected cancer, the particularly cancers such as breast cancer, colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder cancer, pancreatic cancer, cervical cancer, cancers of the central concer, pancreatic cancer, cervical cancer, cancers of the central concer, pancreatic cancer, cervical cancer, cancers of the central concer, pancreatic cancer, cervical cancer, cancers of the central concer, pancreatic cancer, cervical cancer, cancers of the central concers as hybridisation probes, in chromosome and gene mapping, in concers of the cancer cancer cancer cancer and gene mapping, in the cancer cancer and gene mapping in the cancer cancer cancer and gene mapping in the cancer 
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Sequence 2177 B₽; 602 A; 539 C; 605 G; 431 T; 0 ä 0 Other,

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ABI99383 standard; CDNA; 2188

07-MAR-2002 (first entry)

Mouse; ischaemia; compressive ischaemia; occlusive ischaemia; vasospastic ischaemia; ischaemic condition; ischaemic disease; Mouse ischaemic condition related cDNA sequence SEQ Ħ NO:288

88.

WO200188188-A2

22-NOV-2001.

18-MAY-2001; 2001WO-JP004192

18-MAY-2000; 2000JP-00145977

(-INYU) AIND NIHON SCHOOL JURIDICAL PERSON

Ishikawa K, Asai S, Takahashi Y, Nagata T,

2002-034733/04.)B; ABB57126.

Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these

2; Page 794-799; 2690pp; English

ARESULT 12
ARE199383
ID ARE199
AC ARE190
AC AR The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (AB199202 to AB199912, encoding the protein sequences in AB857020 to ABB57374) or by determining the expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an expression as an the

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Matches 1987;
                                                                                                                                                                                                                                                       The present invention relates to novel human secretory or membrane proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-ADA54071). The coding sequences are useful in the gene therapy of diseases caused by abnormalities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic; Gene Therapy; human; secretory protein; membrane proteins; cancer; inflammatory disease; osteoporosis; neurological disease; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                 New polynucleotides encoding full-length polypeptides, e.g. secretory and/or membrane proteins, useful for developing medicines for diseases which the gene is involved, or as target molecules for gene therapy.
                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yamamoto
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24-JAN-2002; 2002US-0350435P.
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bto J, Isono Y,
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ATATGCACAGACCACCCAGGCATATGGGGCAACAAAGCTATGGAACCTATGGACAGCCCAC

186 120 126 60 66

246 180 CTATAGCCAAGCTGCAGCGCAGCAGGGCTACAGTGCTTACACCGCCCAGCCCAGCCCAAGG

CTATAGCCAAGCTGCAGCGCAGCAGGGCTACAGTGCTTACACCGCCCAGCCCACTCAAGG

AGACGGACGTTGAGAGAACGAGGAGGAACGAGAGAAAATGGCGTCCACGGATTACAGTAC

AGACGGACGTTGAGAGAACGAGGAGGAAGGAGAAAATGGCGTCCACGGATTACAGTAC

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67

Query Match Best Local Sin Matches 1984;

Similarity

74.6%;

Score 1782.8; Pred. No. 0; 0; Mismatches

Conservative

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Indels 156; Length 2026; Other;

Gaps

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Sequence

2026 BP;

540 A; 513 C; 590 G; 383

T; 0 U; 0 ВB 42; 13;

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CC This invention relates to novel, isolated full length human cDNA CC molecules and the encoded proteins thereof. Specifically, it refers to CC cDNA clones obtained by an oligo-capping method, where none of these CC clones are identical to any known human mRNAs. The present invention CC describes an immunoassay to identify agonists and antagonists, as well as CC antibodies, antisense molecules and siRNAs that can all be used to bind CC to and modulate expression of the cDNA molecules. As such, these CC the various diseases or morbid states. In particular, they are useful in CC gene therapy for treating osteoporosis, neurological disease, Altheimer's CC disease, Parkinson's disease, dementia, short memory and various cancers, as well as for maintaining equilibrium of sense or motor function, and CC as well as for maintaining equilibrium of sense or motor function, and CC they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian, CC cytostatic and tranquiliser activities. This polymucleotide is a full CC cytostatic and tranquiliser activities. This polymucleotide is a full CC cytostatic and tranquiliser activities. This polymucleotide is a full CC cytostatic and tranquiliser activities. This polymucleotide is a full CC cytostatic and tranquiliser activities. This polymucleotide is a full CC cytostatic conductor of the invention. NOTE: This sequence is not CC co-ROM from the European Patent Office, Vienna Sub-office.
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Wakamatsu A,
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09-MAY-2003; 2003JP-00131452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New 1995 cDNA, useful Alzheimer's diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 952; 2686pp; English.
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Human PRO cDNA sequence SEQ ID NO: 2309

human; PRO; immune related disease; inflammatory immune response;

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                                                                                                                                                                                 The present invention describes an isolated PRO nucleic acid (1). Also CC described: (1) a vector comprising (1); (2) a host cell comprising the vector of (1); (3) a process for producing a PRO polypeptides; (4) an CC isolated PRO polypeptide; (5) a chimeric molecule comprising the CC polypeptide of (4) fused to a heterologous amino acid sequence; (6) an CC antibody which specifically binds to a polypeptide of (4); (7) a CC composition of matter comprising a polypeptide of (4), an agonist or CC polypeptide in combination with a carrier; (8) an article of manufacture comprising a container, a label on the container and a composition of CC matter of (7); (9) a method of treating an immune related disease in a CC mammal; (10) a method for determining the presence of a PRO polypeptide (1) a sample suspected of having the polypeptide; (11) a method of CC diagnosing an immune related disease or an inflammatory immune response CC in mammal; (12) a method of identifying a compound that inhibits or CC minics the activity of or expression of a gene encoding a PRO polypeptide (2); and (13) a method of stimulating the immune response in a mammal; (12) a method of stimulating the immune response in a PRO polypeptide (2); and (13) a method of stimulating the immune response in a mammal. The CC antiasthmatic, antitabletic, antiinflammatory, antiarthritic, CC antiasthmatic, antitabletic, antiantant, immunesuppressive, muscular, CC that the encoded polypeptide, immunostimulant, immunosuppressive, muscular, cephrotropic, neuroprotective, osteopathic, respiratory, vasotropic and CC ill and the encoded polypeptides, compositions, kits and methods are useful in diagnosing and treating an immune related disease and in CC productide sequence from the present sequence represents a human CC productide sequence from the present invention.
                                                                                                                    Query Match
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Matches 1794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New PRO polynucleotides and polypeptides, useful in useful in diagnosing and treating an immune related disease, e.g. systemic lupus erythematosus, rheumatoid arthritis, diabetes mellitus or asthma and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immune response stimulation; antiallergic; antianaemic; antiarthritic; antiarthmatic; antithytoid; CNS; dermatological; gastrointestinal; antithyroid; CNS; dermatological; gastrointestinal; haemostatic; hepatotropic; immunostimulant; immunosuppressive; muscular; nephrotropic; neuroprotective; osteopathic; respiratory; vasotropic; virucide; gene therapy; gene; ss.
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                                         AGGATTAAATGACAGTGTGACTCTAGATGATCTGGCAGACTTCTTTAAGCAGTGTGGGGT
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GCACCGTCAGGAGCGCAGAGATCGGCCCTACTAG 2014 	1981 GC 1774 GC	\$ \$
GGAACAGATGGGAGGAAGAAGAGGAGGACGTGGAGGACCTGGAAAAATGGATAAAGGCGA 	1921 GG 1714 GG	B 8
CCGAGGTGGCTTTGGTGGAGGAAGACGAGGTGGCCCTGGGGGGGCCCCCTGGACCTTTGAT	1861 CC - 1654 CC	B 8
AATGTTCAGAGGTGGCCGTGGTGGAGACAGAGGTGGCTTCCGTGGTGGCCGGGGCATGGA	1801 AA - 1594 AA	문 &
TGGCCCTGGTGGCATGCGGGGAGGAAGAGACGTGGCCTCATGGATCGTGGTGGTCCCGGTGG	1741 TG - 1534 TG	용 성
AAAGCCTGAAGGCTTCCTCCCGCCACCCTTTCCGCCCCCGGGTGGTGATCGTGGCAGAGG	1681 AA - 1474 AA	용 성
TCCGGGTTGTGGAAACCAGAACTTCGCCTGGAGAACAGAGTGCAACCAGTGTAAGGCCCC 1680 	1621 TC - 1414 TC	B 8
AGGGAACCCCTCTGGAGGAGGAAACGTCCAGCACCGAGCTGGAGACTGGCAGTGTCCCAA	1561 AG 1354 AG	유 성
CATGGGAGGCCGTGGAGGAGATAGAGGAGGCTTCCCTCCAAGAGGACCCCGGGGTTCCCG 15	1501 CA 1294 CA	문 왕
GCCACCACTACTGGAGGTCCAGGAGGCCCAGGAGGTCCTGGGGGACCCATGGGTCG 15	1441 GC - 1234 GC	유 성
GAAGAAGCCTCCAATGAÁCAGTATGCGGGGTGGTCTGCCACCCCGTGAGGGCAGAGGCAT 1440 	1381 GA 1174 GA	용 성
CGTGGAATGGTTTGATGÓGAAAGATTTTCAAGGGAGCAAACTTAAAGTCTCCCTTGCTCG 1380 	1321 CG 	B 8
AGGAAAGCCCAAAGGCGATGCCACAGTGTCCTATGAAGACCCACCC	1261 AG - 1054 AG	유 성
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/EG_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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                     GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
   BB
US-08-343-443B-1
US-09-949-016-13696
US-09-949-016-5043
US-09-949-016-1954
US-09-949-016-16785
US-09-949-016-16786
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US-09-949-016-66382
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US-09-621-976-13061
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             Sequence 1, Appli
Sequence 5043, Ap
Sequence 5044, Ap
Sequence 1954, Ap
Sequence 18, Appl
Sequence 16785, A
Sequence 16785, A
Sequence 1657, Appl
Sequence 13361, A
Sequence 13361, A
Sequence 1366, Ap
Sequence 17662, A
Sequence 176641,
Sequence 176637,
Sequence 176637,
Sequence 176633,
Sequence 176645,
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Sequence 4, Appl			Sequence 16775,		Sequence 13765, A	Sequence 12052, A	Sequence 416,	Sequence 1, Appli	Sequence 19, Appl	Sequence 176663	Sequence 176640	Sequence 14,	Sequence 5928	Sequence 12371	Sequence 13845,	Sequence 315	Sequence 3, Appli

ALIGNMENTS

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US-08-343-443B-1
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TYPE: nucleic acid
STRANDENNESS: double
TOPOLOGY: linear
FEATURE:
FEATURE:
NAME/KEY: CDS
LOCATION: 25.1992
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Query Match Best Local Similarity 96.4%; Pred. No. 0; Matches 2106; Conservative 0; Mismatches 76; Indels 2; Gaps 2; Qy 6 GAGACGGACGTTGAGAGAACGAGGAGAAAATGGCGTCCACGGATTACAGTA 65	; NUMBER OF SEQ ID NOS: 207012 ; SOPTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 13696 ; LENGTH: 6002 ; TYPE: DNA ; ORGANISM: Human US-09-949-016-13696	01307 NUMBER: US/09/949,016 : 2000-04-14 UMBER: 60/241,755 2000-10-20 UMBER: 60/237,768 2000-10-03 2000-10-03 MBER: 60/231,498	RESULT 2 US-09-949-016-13696 US-09-949-016-13696; Application US/09949016 Patent No. 6812339 Patent INFORMATION: APPLICANT: VENTER, J. Craig et al. APPLICANT: VENTER, J. Craig et al. TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF	Db 2281 TCTTÄÄCTGTÄÄCAATGTTCATGGTTGTGATGTTTTTTTTTT	Db 2221 TTTAACAATGGTTCATGGTTGTGAGCATTTTTTTTTTTT	2180 TTAAATGGTAGTGTGCGGAGTTTTTTTTTCTTCCTTCTTTTAAAAATGGTTGTTTAAGAC	Db 2041 TARACCAGARARGTTTTARATTTATAATTCCATATTTATAATGTTGGCCACAACATTAT 2100 Qy 2120 GATTATTCCTTGTCTGTACTTTAGTATTTTTCACCATTTGTGAAGAACATTAAAACAAG 2179	
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GAGAGCAAGTTGGCTTCAATAAGCCTGGTGGACCCATGGATGAAGGACCAGATCTTGATC TAGGCCCACCTGTAGATCCAGATGAAGACCTCTGACAACAGTGCAATTTATGTACAAGGAT TAGGCCCACCTGTAGATCCAGATGAAGACTCTGACAACAGTGCAATTTATGTACAAGGAT TAGGCCCACCTGTAGATCCAGATGAAGACTCTGACAACAGTGCAATTTATGTACAAGGAT TAGGCCCACCTGTAGATCCAGATGAAGACTCTGGCACACAGGGAATTTATGTACAAGGAT TAGAACAGATGATCCAGATGAACTCGGCAGACTTCTTTAAGCAGTGTGGGGTTGTTA TAGAACAAGACAGTGTGACTCTAGATGATCCGCAGACTTCTTTAAGCAGTGTGGGGTTGTTA AGATGAACAAGAACTGGGCAACCCATGATCCACACTCTACTGACAAGGAAACAAGGAA AGATGAACAAGAGAACTGGGCAACCCATGATCCACACTCACCTGGACAAGGAAACAAGAA AGATGAACAAGAGAACTGAGCCAATGATCCACACTCACCTGCCAAGGCTGCCGTGG AGATGAACAAGAGAACTGAGCCCAAGGCCCAACGCTGCCGTGGAAACAAGAAACAAGAAAAGAGCAAGGAAACAAGAAACAAGAAAAGACTTAAAAGGTGATGCCACAGGTTGCTCCGTGAAGAACAAGAAAAGATTTTCAAGGGGAACCTTAAAAGTCTCCCTTGCTCGGAAAGAAA	06 CAGARAGAACCGGAGCATGAGTGGCCTGATAACCGGGGAGAGGGAAGAGGGGATTTG 965		ACTOTCAGCAGAACACCTATGGGCAACCGAGCAGCTATGGACAGCAGAGTAGCTATGGTC 725				AGCCTGTCCAGGGGTATGGCACTCGGTGCTTATGATACCACCACCACCACCTGCTTATCAGCCTATGCAGCCTATGCAGCCTATGCAGCCTATGCAGCCTATGCAGCCTATGCAGCCTATGCAGCCTATGCAGCCTATGCAGCCTATGCAGCCTATGCAGCCTATGCAGCCTATGCAGCCTATGCAGCCTATGCAGCCTATGCAGCCTATGCAGCCTATG	46 CTTCTTATGGACAGCCTCCCACTGGTTATACTACTCCAACTGCCCCCAGGCATACAGCC 305

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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
                                                                                                                   Sequence 5043, Application Patent No. 6812339
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PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR PPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.
SEQ ID NO 5043
LENGTH: 1785
TYPE: DNA
ORGANISM: Human
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APPLICATION: VENTER, J. Craig et al.
APPLICATION: POLYMORPHISMS IN KNOWN GENES ASSITITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR REPLICATION NUMBER: 60/231,498
PRIOR RILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOPTWARE: FRASTSEQ for Windows Version 4.0
SEQ ID NO 5044
LENGTH: 1785
TYPE: DNA
ORGANISM: Human
US-09-949-016-5044
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Patent No. 6812339
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GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION A

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08
SOFTWARE: FastSEQ for Windows
SEQ ID NO 1954
LENGTH: 1783
TYPE: DNA
ORGANISM: Human
US-09-949-016-1954
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                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Landanyi, Marc
APPLICANT: Gerald, William
ITILE OF INVENTION: A DIAGNOSTIC TE
TITLE OF INVENTION: SMALL ROUND CEI
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                              Sequence 18, Application US/08437027 Patent No. 5670317
        ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,027
FILING DATE:
TILING DATE:
 CLASSIFICATION:
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GAGCGCAGAGATCAGCCCTACTAG
                                                                                                       GGAGGAAGAAGAGGACGTGAAGGACCTGGAAAAACGGATAAAGGCGAGCACTGTCAG
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TELEPHONE: 212-278-0400
TELEPHONE: 212-391-0525
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 2412 base pairs
TYPE: nucleic acid
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NAME: White, John P
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 46416/JPW/CCA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
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Similarity 100.0%; Pred. No. 2.5e-206;
19; Conservative 0; Mismatches 0; Indels
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CAATATAGCCAACAGAGCAGCAGCTACGGGCAGCAGAGT 838
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                                                                      GGGCAGCAGCCTCCCACTAGTTACCCCACCCCAAACTGGATCCTACAGCCAAGCTCCAAGT 799
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PRIOR PRICATION NUMBER: 60/237,768
PRIOR PRIOR PRICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FABLSEQ for Windows Version 4.0
SEQ ID NO 16785
LENGTH: 35784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LENGTH: 35784
; TYPE: DNA
; ORGANISM: Human
; ORGANISM: Human
US-09-949-016-16785
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Patent No. 6812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 665; Conserv
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
CUCRENT ADDITIONAL
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                                                               GAGCTGCATTGACTACCAGATTTATTTTTAAACCAGAAAATGTTTTAAATTTATAATTC
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                                                                                                                                                                                                                                                                                  GTCCTCATGTCTCTAGGAAGCTTGTGATAGTGGTTGGGAGGAGCCAGGAAGGGGCACCTG 33680
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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Pred. No. 4.1e-103;
0; Mismatches 19;
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OF DETECTION AND USES THEREOF
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Query Match Best Local (

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MOLECULE TYPE: cDNA to mRNA

TOPOLOGY:

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STRANDEDNESS: single

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721 740 661 089 601 541 560 481

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Title:
Perfect score:
Sequence:
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Maximum DB seq length: 200000000
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Maximum Match 100%
Listing first 45 s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
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9 US-09-822-830A-49
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Sequence 1, Appli
Sequence 3769, Ap
Sequence 1081, App
Sequence 717, App
Sequence 410, App
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sequence 1576, Ap	244/0,	Sequence 2865, Ap	Sequence 19297, A	Sequence 322, App						111655	Sequence 8052, Ap	17973		Sequence 2572, Ap	Sequence 297, App	Sequence 25438, A	18163,	e 4463		Sequence 481, App	Sequence 3851, Ap	σ		31212		Sequence 124982,	æ	10259	Sequence 24705, A	e 3868	766,	19709,	Sequence 9557, Ap

ALIGNMENTS

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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 2390
TYPE: NAME
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TYPE: DNA
ORGANISM: Homo mapiens
FEATURE:
NAME/KBY: CDS
LOCATION: (44)..(2011)
OTHER INFORMATION: EWS
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TITLE OF INVENTION: Methods for Determining Hormonal Effects of Substances
FILS REPERSUE: Pat 3684/11
CURRENT APPLICATION NUMBER: US/10/791,017A
CURRENT FILING DATE: 2004-03-02
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Sequence 3769, Application US/09880107

Patent No. US20020142981A1

GENERAL INFORMATION:

APPLICANT: Horne, Darci T.

APPLICANT: Vockley, Joseph G.

APPLICANT: Scherf, Uwe

APPLICANT: Gene Logic, Inc.

TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer

PILE REFERENCE: 44921-9028-W0

CURRENT FILING DATE: 2001-06-14

PRIOR APPLICATION NUMBER: US 60/211,379

PRIOR APPLICATION NUMBER: US 60/211,379

PRIOR APPLICATION NUMBER: US 60/237,054

PRIOR PILING DATE: 2000-10-614

PRIOR PILING DATE: 2000-10-62

NUMBER OF SEQ ID NOS: 3950

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 3769

LENGTH: 2390

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: Genbank Accession No. US20020142981A1 X66899

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APPLICANT: Munger, William E:
TITLE OF INVENTION: Identifying Drugs for and Diagnosis of
TITLE OF INVENTION: Gene Expression Profiles
FILE REFERENCE: 44921-5029-01US
CURRENT APPLICATION NUMBER: US/09/960,706
CURRENT FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: 60/223,323
PRIOR FILING DATE: 2000-08-07
PRIOR APPLICATION NUMBER: 60/223,319
PRIOR APPLICATION NUMBER: 60/23,319
PRIOR FILING DATE: 2001-06-05
NUMBER OF SEQ ID NOS: 1124
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1081
LENGTH: 2390
TYPE: DNA
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; Sequence 1081, Application US/09960706
; Publication No. US20030134280A1
; GENERAL INFORMATION:
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APPLICANT: Munger, William E.
APPLICANT: Munger, William E.
APPLICANT: Munger, William E.
APPLICANT: Maga, Iwao
APPLICANT: Waga, Iwao
APPLICANT: Yamamoto, Jun
TITIE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Pros
TITLE OF INVENTION: IPPERPLAGATE USING Gene Expression Profiles
FILE REFERENCE: 44921-5029-US
CURRENT APPLICATION NUMBER: US/09/873,319A
CURRENT FILLING DATE: 2001-06-05
EARLIER APPLICATION NUMBER: US 60/223,323
EARLIER FILLING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 755
SOPTWARE: Patentin Ver. 2.1
SEQ ID NO 717
LENGTH: 2390
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
ORGANISM: Homo sapiens
FEATURE: INFORMATION: Genbank Accession No. US20030134324A1 X66899
US-09-873-319-717
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US-09-873-319-717
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Best Local Similarity
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99.9%; Score 2388.4;
100.0%; Pred. No. 0;
tive 0; Mismatches
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APPLICANT: AGOSTINO, MICHAEL J.
APPLICANT: Howes, Steven H.
APPLICANT: Resnick, Richard J.
APPLICANT: Gulukota, Kamalakar
APPLICANT: Graham, James R.
ITITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECTORENT APPLICATION NUMBER: US/09/822,830A
CURRENT FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/195,604
PRIOR APPLICATION NUMBER: 60/195,604
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 631
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 410
LENGTH: 2273
TYPE: DNA
ORGANISM: Homo sapiens
US-09-822-830A-410
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; GENERAL INFORMATION:
; APPLICANT: Genetics Institute, Inc.
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Agostino, Michael J.
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Matches 2259; Conservat
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                             CGACTAGTTATGATCAGAGCAGTTACTCTCAGCAGAACACCTATGGGCAACCGAGCAGCT
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APPLICANT: Genetics Institute, Inc.
APPLICANT: Wong, Gordon G.
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APPLICANT: Wong, Gordon G.
APPLICANT: Hosel, Kim
APPLICANT: Agostino, Michael J.
APPLICANT: Agostino, Michael J.
APPLICANT: Resnick, Richard J.
APPLICANT: Gulukota, Kamalakar
APPLICANT: Gulukota, Kamalakar
APPLICANT: Graham, James R.
ITITLE OF INVENTION: POLYMUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
FILE REFERENCE: GIN 6402
CURRENT APPLICATION NUMBER: US/09/822,830A
CURRENT FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/195,604
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 631
SOPTWARE: Patentin Ver. 2.0
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US-09-822-830A-49/c
IS-09-822-830A-49/c
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; Patent No. US20020142952A1
; GENERAL INFORMATION:
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APPLICANT: HIO, YUKI
APPLICANT: OTSUKA, KAORU
APPLICANT: HRIE, RYOTANO
APPLICANT: TRIE, RYOTANO
APPLICANT: SEKI, NAOTOYUKI
APPLICANT: SEKI, NAOTOYUKI
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: MASUHO, YASUHIKO
APPLICANT: MASUHO, YASUHIKO
ITILE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR RILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR FILING DATE: 2001-09-14
NUMBER OF ESQ ID NOS: 3381
SOFTWARE: PATENTIN VET. 2.1
SOFTWARE: PATENTIN VET. 2.1
SOFTWARE: PATENTIN VET. 2.1
CORGANISM: Homo sapiens
US-10-094-749-1074

75.7%; Score 1808
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Publication No. US20030219741A1
GENERAL INFORMATION:
APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOVASU
APPLICANT: SUGIYAMA, TOMOVASU
APPLICANT: WAKAWATSU, AI
APPLICANT: WAKAWATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: SHIJI SHIZUKO
APPLICANT: YAMAWOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
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Best Local Similarity 92.2%;
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HIO, YURI
                                                                                                    CATATGGCACTCAGCCTGCTTATCCAGCCTATGGGCAGCAGCAGCAGCAGCCACTGCACCTA 452
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                   CAAGACCGCAGGATGGAAACAAGCCCACTGAGACTAGTCAACCTCAATCTAGCACAGGGG
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ACCGAGCTGGAGACTGGCAGTGTCCCAATCCGGGTTGTGAAACCAGAACTTCGCCTGGA 1652
                                                                                                                                          CAGGAGGTCCTGGGGGACCCATGGGTCGCATGGGAGGCCGTGGAGGAGATAGAGGAGGCCT 1532
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RESULT 8 US-10-425-115-182496 ; Sequence 182496, Application US/10425115 ; Publication No. US20040214272A1

GENERAL INFORMATION:

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; OTHER INFORMATION: US-10-425-115-182496
Query Match
Best Local S
Matches 661
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 18246
LENGTH: 763
                                                                                                                          TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(763)
OTHER INFORMATION: un
                                                                                                             FEATURE:
   661;
                   Similarity
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                   26.4%;
Score 631; DB 18;
Pred. No. 9.9e-151;
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37.8	37.8	37.8	37.8	37.8	37.8	37.9	37.9	37.9	38.0	38.1	38.2	38.4	38.4	38.4	38.5	38.5	38.6	38.7	38.8	38.8
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BX428312	BX399070	BX420692	BX424687	BX449773	BX429003	BX407870	BX381313	BQ059077	BX443095	BX407826	BX382091	BX421725	BM468711	BM802924	BQ059127	BM477969	BX353312	BX449774	BQ062138	BM927718
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ALIGNMENTS

ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS REFERENCE AUTHORS TITLE JOURNAL REMARK RESULT 1 CR608375 LOCUS S 뭐 ORIGIN FEATURES COMMENT DEFINITION Query Match Best Local Sim Matches 2314; TITLE JOURNAL source Direct Schmission

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECOR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. 4 GGGAGACGGACGTTGAGAGAAACGAGGAAGGAAGAAAAATGGCCGTCCACGGATTACAG Contact : Feng Liang Email : fliar http://fulllength.invitrogen.com/ Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2314)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Poll-length cDNA libraries and normalization CR608375 2314 bp mRNA linear full-length cDNA clone CS0DI039YJ24 of Placenta Cot of Homo sapiens (human). Faraday Avenue 2 (bases 1 to 2314) Unpublished CR608375.1 GI:50489182 HTC; CNSLT_cDNA. Genoscope Homo sapiens Homo sapiens (human) Similarity GGGAGACGGACGTTGAGAGAACGAGGAGGAAGGAGAGAAAATGGCGTCCACGGATTACAG Conservative /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODIO394724"
/tissue_type="Placenta_Cot_29
/plasmid="pCMVSPORT_6" Location/Qualifiers . .2314 96.8%; Score 2314; I 100.0%; Pred. No. 0; Live 0; Mismatches Email : fliang@lifetech.com URL vitrogen.com/ InVitroGen Corporat B 25-normalized" ω --0 Length 2314; Indels Corporation 1600 HTC 21-JUL-2004 25-normalized 0 Gape 60 0

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2164 GAAACATTAAAACAAGTTAAATGGTAGTGTGCGGAGTTTTTTTT	2104 TTGGCCACAACATTATGATTATTCCTTGTCTGTACTTTAGTATTTTTCACCATTTGTGAA 2163 	2044 TACCAGATTTATTTTTAAACCAGAAAATGTTTTAAATTTATAAATTCCATATTTATAAATG 2103 	1984 CCGTCAGGAGCGCAGAGATCGGCCCTACTAGATGCAGAGACCCCCGCAGAGCTGCATTGAC 2043	1924 ACAGATGGGAGGAAGAAGAGGAGGACGTGGAGGACCTGGAAAAATGGATAAAGGCGAGCA 1983 	1864 AGGTGGCTTTGGTGGAGGAAGACGAGGTGGCCCTGGGGGGGCCCCCTGGACCTTTGATGGA 1923 	1804 GTTCAGAGGTGGCCGTGGTGGAGACAGAGGTGGCTTCCGTGGTGGCCGGGGCATGGACCG 1863 	1744 CCCTGGTGGCATGCGGGGAGGAAGAGGTGGCCTCATGGATCGTGGTGGTCCCGGTGGAAT 1803 	1684 GCCTGAAGGCTTCCTCCCGCCACCCTTTCCGCCCCCGGGTGGTGATCGTGGCAGAGGTGG 1743 	1624 GGGTTGTGGAAACCAGAACTTCGCCTGGAGAACAGAGTGCAACCAGTGTAAGGCCCCAAA 1683 	1564 GAACCCCTCTGGAGGAGGAAACGTCCAGCACCGAGCTGGAGACTGGCAGTGTCCCAATCC 1623 	1504 GGGAGGCCGTGGAGGAGATAGAGGAGGCTTCCCTCCAAGAGGACCCCGGGGTTCCCCAAGA 1563 	1444 ACCACCACTCCGTGGAGGTCCAGGAGGCCCAGGAGGTCCTGGGGGACCCATGGGTCGCAT 1503	1384 GAAGCCTCCAATGAACAGTATGCGGGGTGGTCTGCCACCCCGTGAGGGCAGAGGCATGCC 1443 	1324 GGAATGGTTTGATGGGAAAGATTTTCAAGGGAGCAAACTTAAAGTCTCCCTTGCTCGGAA 1383 	1264 AAAGCCCAAAGGCGATGCCACAGTGTCCTATGAAGACCCACCC	1204 TAAGATGAACAAGAGAACTGGGCAACCCATGATCCACATCTACCTGGACAAGGAAACAGG 1263 	1144 ATTAAATGACAGTGTGACTCTAGATGATCTGGCAGACTTCTTTAAGCAGTGTGGGGGTTGT 1203

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                                                                                        Eukaryota; Metazoa; Chordata; C. Mammalia, Eutheria; Primates; C. 1 (bases 1 to 2236)
Li,W.B., Gruber,C., Jessee,J. a: Full-length cDNA libraries and Unpublished
Faraday Avenue
2 (bases 1 to 223
Genoscope.
Direct Submission
                                                                                                                                                                                                                      CR604639 2236 bp mRNA line full-length cDNA clone CSODJ013YN08 of T cells Cot 10-normalized of Homo sapiens (human). CR604639 GR604639.1 GI:50485446 HTC; CNSLT_CDNA.
                                                           Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation
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- Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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/mol_type="mRNA"
/db xref="taxon:9606"
/clone="CSODJO13YN08"
/tissue_type="T cells (Jurkat c. 10-normalized"
/plasmid="pCMVSPORT_6"
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/tissue_type="Placenta" /tissue_type="Placenta" /plasmid="pCMVSPORT_6"	/organism="Homo sapiens" /mol_type="mRNA" /db xref="taxon:9606" /clone="rcsnpx06ver1"		Tal med	Genoscope. Genoscope. Direct Submission Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr	Contact: Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue 2 (bases 1 to 2159)	to 2159) to 2159) uber, C., Jessee, J. cDNA libraries an	sapiens (human sapiens sapiens ryota; Metazoa;	(human). (R625247 CR625247.1 G1:50506054	CR625247 2159 bp mRNA linear HTC 21-JUL-2004	306 CHSIANCAA ISIICA ISSIISISAIS 2331 		SOLANDIA DECENSO IL	CCTA CHOCOCCO CHEMINATITATICA CONTROLLA & A RECONTROLLA & CA CHITTA A C	ACCOMPANY OF THE ACCO	CCCIACIANA ISCANDACICCONAMENTA INCICIACIANA INCICIACIANA INCICATA	COLE E ELEMENTE ELEMENT DE LO COLO DEL LO COLO DE LO COLO DEL LO COLO DEL LO COLO DEL LO COLO DE LO COLO DE LO COLO DEL LO COLO		886 CGAGGTGGCCCTGGGGGGCCCCCTGGACCTTTGATGGAACAGATGGGAGGAAGAAGAGAGA 1945

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Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2126)
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Full-length cDNA libraries and normalization
Unpublished
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2 (bases 1 to 2126)
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   CCAGCCTATGGGCAGCAGCCAGCAGCCACCTACAAGACCGCAGGATGGAAACAAG
                                                    GTCACCACCCAGGCCTCCTATGCAGCTCAGTCTGCATATGGCACTCAGCCTGCTTAT
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODP037Y107"
/tissue_type="Fetal brain"
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Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five primer
                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo 1 (bases 1 to 2103)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished CONTact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ InvitroGen Corporation
                                                                                                                                                                                                             CR619493 2103 bp 1 full-length cDNA clone CS0DI076YO21 of Homo sapiens (human). CR619493 CR619493.1 GI:50500300 HTC; CNSLT_CDNA.
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/clone="CSODIO76Y021"
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CR608666
full-length cDNA clone Cleone Cleone Sapiens (human).
CR608666
CR608666.1 GI:50489473
HTC; CNSLT_cDNA.
Homo sapiens (human)
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1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a
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1 (bases 1 to 2083)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Pull-length cDNA libraries and normalization

Unpublished
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Location/Qualifiers
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Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_Tref="texon:9606"
/clone="CSODG004YL23"
/tissue_type="B cells (Ramos cuplasmid="pCMVSPORT_6"
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1113 ACTCTGACAACAGTGCAATTTATGTACAAGGATTAAATGACAGTGTGACTCTAGATGATC	273 ATNCTNCTCCALCTGCCCCCCAAGCATNCDGCCAGCCTGTCCAGGGGTATGGCACTGGTG 322 181 ATNCTNCTCCALCTGCCCCCCCCCCAGGATACAGCCCCCCCAGGGCTATGGCACTGGTG 322 181 ATNCTNCTCCALCTGCCCCCCCCCCAGGATCAGCCCCCCCCCCCCC
RESULT 8 CR594868 CR594868 CR594868 CR594868 CR594868 CR594868 CR594868 VERSION CR594868.1 GI:50475675 KXYWORDS HTC; CNSLT CNNA. SOURCE ORGANISM Homo sapiens (human) ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hom ITILB JOURNAL REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :	Db 1261 GBACCHACTTRANGTTCCCTTGCTGGAANGANAGCCTTCCCAATGAACTTANAGTTCAATGAACATTANAAAAAAAAAA

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AA 2083	CTGTACTTTAGTATTTTTCACCATTTGTGAAGAAACATTAAAA)b 2041
AA 2175	CTGTACTTTAGTATTTTTCACCATTTGTGAAGAAACATTAAAA	
CATTATGATTATTCCTTGT 2040	1 GTTTTAAATTTATAATTCCATATTTATAATGTTGGCCACAACATTATGATTATTCCTTGT)b 1981
CATTATGATTATTCCTTGT 2132		<i>y</i> 2073
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ATTTTTAAACCAGAAAAT 2072)y 2013
CGCAGAGATCGGCCCTACT 1920)b 1861
CGCAGAGATCGGCCCTACT 2012	3 GAGGACCTGGAAAAATGGATAAAAGGCGAGCACCGTCAGGAGCGCAGAGATCGGCCCTACT	ን ሃ 19 5
GGAAGAAGAGGAGGACGTG 1860)b 1801
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ATGCGGGGAGGAAGAGGTG 1772	3 CGCCCCCGGGTGGTGATCGTGGCAGAGGTGGCCCTGGTGGCATG)y 171
TTCCTCCCGCCACCCTTTC 1620	1 GAACAGAGTGCAACCAGTGTAAGGCCCCAAAGCCTGAAGGCTTC)b 156
TTCCTCCCGCCACCCTTTC 1712	3 GAACAGAGTGCAACCAGTGTAAGGCCCCAAAGCCTGAAGGCTTCCTCCCGCCACCCTTTC	<i>l</i> y 165
AACCAGAACTTCGCCTGGA 1560	1 ACCGAGCTGGAGACTGGCAGTGTCCCCAATCCGGGTTGTGGAAACCAGAACTTCGCCTGGA)b 1501
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GGAGGAGGAAACGTCCAGC 1500	1 TCCCTCCAAGAGGACCCCGGGGTTCCCGAGGGAACCCCTCTGGAGGAAGGA	b 1441
GGAGGAGGAAACGTCCAGC 1592	3 TCCCTCCAAGAGGACCCCGGGGTTCCCGAGGGAACCCCTCTGGA	ly 153
GGAGGAGATAGAGGAGGCT 1440	1 CAGGAGGTCCTGGGGGGACCCATGGGTCGCATGGGAGGCCGTGGAGGAGATAGAGGAGGCT)b 1381
GGAGGAGATAGAGGAGGCT 1532		ly 1473
CGTGGAGGTCCAGGAGGCC 1380	1 GTCTGCCACCCCGTGAGGGCAGAGGCATGCCACCACCACCACTCCGTGGAGGTCCAGGAGGCC	b 132
CGTGGAGGTCCAGGAGGCC 1472		y 1413
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Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was disted with Not I and cloned into the Not I and EcoR V sites of the pcMvSpORT 6 vector. Library was normalized, Library was constructed by Life Technologies, a division of Invitrogen.
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Genoscope.
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CCCACTGAGACTAGTCAACCTCAATCTAGCACAGGGGGTTACAACCAGCCCAGCCTAGGA
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                                                                                         ACTGCACCTCCATCCTACCCTCCTACCCAGCTATTCCTCTACACAGCCGACTAGTTATGAT
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/clone="CSODIO64YE15"
/tissue_type="Placenta Cot
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	FEATURES SOUICE	REFERENCE AUTHORS TITLE JOURNAL COMMENT	VERSION KEYWORDS SOURCE ORGANISM REPERENCE AUTHORS TITLE JOURNAL	RESULT 9 CR593724 LOCUS DEFINITION ACCESSION	B &	B 8	D Q	P Q	₽ &
/ Match 86.7%; Score 2073; DB 3; Length 2073; Local Similarity 100.0%; Pred. No. 0; Les 2073; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 93 GCTACAGTGCTTACACCGCCCAGCCCATCAAGGATATGCACAACCACCCAGGCATATG 152	into was div.			CR593724 2073 bp mRNA linear HTC 21-JUL-2004 DN full-length cDNA clone CS0DI011Y005 of Placenta Cot 25-normalized of Homo sapiens (human).	2096 TYATAATGTTGGCCACAACATTATGATTATTCCTTGTCTGTACTTTAGTATTTTTC 2151	2036 GCATTGACTACCAGATTTATTTTTTAAACCAGAAAATGTTTTAAATTTATAATTCCATAT 2095	1976 GGCGAGCACCGTCAGGAGCGCAGAGATCGGCCCTACTAGATGCAGAGACCCCGCAGAGCT 2035	1916 TTGATGGAACAGATGGGAAGAAGAAGAAGAAGGACGTGGAAGAACTGGAAAAATGGATAAA 1975 	1856 ATGGACCGAGGTGGCTTTGGTGGAGGAAGACGAGGTGGCCCTGGGGGGGCCCCCTGGACCT 1915
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                                         CR602561 2070 bp mR1 full-length cDNA clone CS0DI068YN23 of of Homo sapiens (human).
CR602561 GI:50483368
HTC; CNSLT_CDNA.
Homo sapiens (human)
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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1st strand cDNA was primed with a NotI-oligo (dT) primer. Five end enriched, double-strand cDNA was digested with Not I and cinto the Not I and ECOR V sites of the pcwVSPORT 6 vector. Litwas normalized. Library was constructed by Life Technologies, division of Invitrogen.

Location/Qualifiers
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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                                               ACTGCACCTCCATCCTACCCTCCTACCAGCTATTCCTCTACACAGCCGACTAGTTATGAT
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODIO68YN23"
/tissue_type="Placenta Cot 2
/plasmid="pCMVSPORT_6"
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ACCCATG 1495 ACCCATG 1437	1436 GGCATGCCACCACCACTCCGTGGAGGTCCAGGAGGCCCAGGAGGTCCTGGGGGACCCATG
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TTCCCTT 1375	1316 GCTGCCGTGGAATGGTTTGATGGGAAAGATTTTCAAGGGAGCAAACTTAAAGTCTC
RGCCAAG 1315 RGCCAAG 1257	1256 GAAACAGGAAAGCCCAAAGGCGATGCCACAGTGTCCTATGAAGACCCACCC
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TGGAGGA 895	836 AGTTCATTCCGACAGGACCACCCCAGTAGCATGGGTGTTTTATGGGCAGGAGTCTGGAGGA
CAGCAG 835	776 GGATCCTACAGCCAAGCTCCAAGTCAATATAGCCAACAGAGCAGCAGCTACGGGC
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The RIKEN Genome Ex FANTOM Consortium. Functional annotati Nature 409, 685-690 5

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Group Phase II Team and

annotation of a full-length mouse cDNA collection , 685-690 (2001)

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REFERENCE ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 11 AK034755 LOCUS REFERENCE AUTHORS DEFINITION TITLE AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000) Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kiteunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Pujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000) AK034755 2373 bp mRNA linear HTC 03-APR-2004 Mus musculus 12 days embryo embryonic body between diaphragm region and neck cDNA, RIKEN full-length enriched library, clone:9430031M11 product:Ewing sarcoma homolog, full insert sequence.

AK034755 Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA Meth. Enzymol. 303, 19-44 (1999) 99279253 AK034755.1 GI:26084174 HTC; CAP trapper. Mus musculus (house mouse) Eukaryota; Metazoa; Mammalia; Eutheria; Mus musculus 11042159 Chordata; Rodentia; Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus lAs to new genes

Query Match B2.8%; Score 1979.8; DB 3; Length 2373; Best Local Similarity 91.8%; Pred. No. 0; Matches 2172; Conservative 0; Mismatches 152; Indels 41; Gaps 6; Qy 5 GGAGACGGACGTTGAGAGAACGAGGAGAAAATGGCGTCCACGGATTACAGT 64	neck" /clone_lib="RIKEN full-length enriched mouse cDNA library" /dev_stage="12 days embryo" misc_feature 432011 /note="Ewing sarcoma homolog (MGD MGI:99960, GB NM_007968, evidence: BLASTN, 99%, match=2172) putative" 23582363 /note="putative" 2373 /note="putative" 2373 /note="putative"	prepare mouse tissues. Please visit our web site for further details. Please visit our web site for further details. URL:http://genome.gsc.riken.jp/ URL:http://fantom.gsc.riken.jp/. Location/Qualifiers /organism="Mus musculus" /mol type="mbNA" /strain="C57BL/6" /db_xref="pANTOM_DB:9430031M11" /db_xref="taxon:10990" /db_xref="taxon:101" /tissue_type="embryonic body between diaphragm region and /tissue_type="embryonic body between diaphragm region and	Direct Submission JOURNAL Submitted (16-UIL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-resegsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9216) COMMENT CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Science Laboratory in RIKEN. Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken Contributed to	AUTHORS The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs JOURNAL 6 (Dases 1 to 2373) REFERENCE 6 (Dases 1 to 2373) AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Haysahida,K., Hayatsu,N., Hirmoto,K., Hirmotoka,T., Kouda,M., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,A., Murata,M., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sogaba,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takada,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M., and Hayashizaki,Y.
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

All Nature 420, 563-573 (2002)

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Trejima,Y., Toya,T., Yamamura,T., Yasunihi,A., Yoshida,K.,

Direct Submission

Submitted (18-AUG-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC),

RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
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High-efficiency full-length cDNA cloning
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Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
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Carminci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                  Mus musculus
Mus musculus
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CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rigenomic Sciences Center and Genome Science Laboratory in RIKEN.
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Analysis of the mouse transcriptome based of 60,770 full-length CDNAs
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Functional annotation of a full-length mouse cDNA collection
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Please visit our web site for further
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  /clone="C530046A18"
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|mol_type="mRNA"
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The RIKEN Genome Exploration Research Group FANTOM Consortium.
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Mammalia; Eutheria; Rodentia;
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Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayateu, N., Hiramoto, K., Hiracka, T., Hori, P., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Koya, S., Kurihara, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sahai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagama, A., Takahashi, P., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIXEN), Laboratory for Genome Exploration Research Group, RIXEN Genomic Sciences Center (GSC), RIXEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoha Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Group Phase I & II Team.
Analysis of the mouse transcriptome of 60,770 full-length cDNAs
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="17 days embryo"
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/protein_id="BAB29301.1"
/db_xref="GI:12852168"
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1049)

1i,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On May 2, 2003 this sequence version replaced gi:30344479.

Contact: Genoscope

Contact: Genoscope
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BX325713 Homo sapiens PLACENTA COT 25 NORMALIZED Homo
clone CSODI039YJZ4 5-PRIME, mRNA sequence.
BX325713
                                                                                                                                                                                                                                                                                               For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSOASO12ZH02QP1&c=10589.f.
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/note="Tist strand cDNA was primed with a NotI-oligo(dT)
/note="Tist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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AC011221 Homo sapi BC068226 Mus muscu AX305537 Sequence X79233 M.musculus	AC137500 Homo sapi AC018774 Homo sapi AL596087 Human DNA	BC011048 Homo sapi BT007796 Synthetic AK056309 Homo sapi CO730352 Semience	A36460 Sequence 1 AR080100 Sequence BC004817 Homo sapi CR456490 Homo sapi BC072442 Homo sapi	CQ867364 Sequence AX411125 Sequence X66899 H.sapiens E	Description

AUTHORS TITLE JOURNAL	SOURCE SOURCE ORGANISM	RESULT 1 CQ867364 LOCUS DEFINITION ACCESSION VERSION	4 5	44.8		41 41			37 101		34		<u>بر</u> د	30	29			25 1625.		23 1652		21	17
Obendorf,M. Modulation Patent: EP Schering Ak	Homo sapiens Homo sapiens Eukaryota; M Mammalia; Eu	CQ867364 Sequence CQ867364 CQ867364.				979	_		1014.4			1302.4			6		n a	ο α	4	.4		0	85.6
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Obendorf,M. and Wolf,S. Modulation of the activity of nuclear Patent: EP 1455190-A 1 08-SEP-2004; Schering Aktiengesellschaft (DE)) Chordata; Crani Primates; Catai	2390 bp t EP1455190. 89	BC063928 ALIGNMENTS	HSU35622 I66247	AK026270	AF254088	AF254086	BC000527	HSM808920	AC118907	AC105889	AU719366	AC113313	CQ721057	AC106522	AC098231	AK12/624	CQ850483	AK056681	AX714390	AC110672	AC109802	BC083960 ·
er receptors	Craniata; Vertebrata; Catarrhini; Hominidae;	DNA																					
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Query Match Best Local	ORIGIN	CDS	AUTHORS TITLE JOURNAL FEATURES BOUICE	KEYWORDS SOURCE ORGANISM REFERENCE	CQ867364 LOCUS DEFINITION ACCESSION VERSION
Query Match 100.0%; Score 2025; DB 6; Length 2390; Best Local Similarity 100.0%; Pred. No. 0;	/codon_gtart=1 /protein_id="CAH33891.1" /brotein_id="CAH33891.1" /db_xref="G1:51997590" /translation="MASTDYSTYSQAAAQQGYSAYTAQPTQGYAQTTQAYGQQSYGTY /translation="MASTDYSTYSQAAAQQGYSAYTAQPTQGYAGTGAXDTTT ATWTTTQASYAAQSAYGTQFAYATSYGQPFAYTFTRPQDGNKFTETSQPQSSTGGYNQ PSILGYGGANYSYPQWFGSYEMQPWTAPFSYEPTSYSSTQFTSYDGSYSQQNWTQGPS SYGQQSSYGQQSFGPGENRSMSGPDNRGGRGGFDGGNGNAFGGRGGRGGGGGGGGGGGGGGGGGGGGGGGGGGG	/organism="nomo sablens" /mol_type="unassigned DNA" /db_xref="taxon:9606" 442014	Obendorf,M. and Wolf,S. Modulation of the activity of nuclear receptors via EWS Modulation of the Activity of nuclear receptors via EWS Patent: EP 1455190-A 1 08-SEP-2004; Schering Aktiengesellschaft (DE) Location/Qualifiers 1. 2390	Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	CQ867364 2390 bp DNA linear PAT 13-SEP-2004 Sequence 1 from Patent EP1455190. CQ867364 CQ867364.1 GI:51997589

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (26-MAY-1992) O. Delattre, Lab. de Genet. des Tumeurs. Inst. Curie, 26 rue D'Ulm, 75231 Paris Cedex, FRANCE On Sep 23, 1994 this sequence version replaced gi:31279.

Location/Qualifiers
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Nature 359 (6391), 162-165 (1992)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                               | Jgene="EWS"
| /codon_start=1
| /product="RNA binding protein"
| /protein_id="CAA47350.1"
| /protein_id="CAA47350.1"
| /protein_id="CAA47350.1"
| /db_xref="G1:31280"
| /db_xre
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/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="22q12"
/clone="BF1AC5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="EWS"
44. .2014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="brain"
/clone_lib="cDNA, Stratagene 936206"
/dev_stage="foetus"
                                                                 LMEQMGGRRGGRGGPGKMDKGEHRQERRDRPY"
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Aurias, A., Delattre, O., Desmaze, C., Melot, T., Peter, M., Plougastel, B., Thomas, G. and Zucman, J.

NUCLEIC ACID CORRESPONDING TO A GENE OF CHROMOSOME 22 INVOLVED RECURRENT CHROMOSOMAL TRANSLOCATIONS ASSOCIATED WITH THE DEVELOPMENT OF CANCEROUS TUMORS
PAtent: WO 9323549-A 1 25-NOV-1993;
CENTRE NAT RECH SCIENT (FR)
Other publication FR 2691475 931126
Other publication JP 8500964T 960206.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Aurias,A., Delattre,O., Desmaze,C., Melot,T., Peter,M.,
Ploougastel,B., Thomas,G. and Zucman,J.
Nucleic acid corresponding to a gene of chromosome 22 involved
recurrent chromosomal translocations associated with the
development of cancerous tumers, and nucleic acids of fusion
resulting from said translocations
Patent: US 5968734-A 1 19-OCT-1999;
Location/Qualifiers
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852 840	793 CAATATAGCCAACAGAGCAGCAGCTACGGGCAGAGTTCATTCCGACAGGACCACCCC
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492 480	433 GCCACTGCACCTACAGACCGCAGGATGGAAACAAGCCCACTGAGACTGAGTCAACCTCAA
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

CE 1 (bases 1 to 2182)

Strausberg, R. L., Feingold, E. A., Grouse, L. H., Derge, J. G., Klausner, R. D., Collins, F. S., Wagner, L., Shenmen, C. M., Schuler, G. D., Altschul, S. F., Zeeberg, B., Buetow, K. H., Schaefer, C. F., Bhat, N. K., Hopkins, R. F., Jordan, H., Moore, T., Max, S. I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A. A., Rubin, G. M., Hong, L., Scheetz, T. B., Boarse, M. B., Bonaldo, M. F., Casavant, T. L., Scheetz, T. B., Brownstein, M. J., Usdin, T. B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S. S., Loquellano, N. A., Peters, G. J., Abramson, R. D., Mullahy, S. J., Bossak, S. A., McEwan, P. J., Malek, J. A., Gunaratne, P. H., Richards, S., Worley, K. C., Hale, S., Garcia, A. M., Gay, L. J., Hulyk, S. W., Villalon, D. K., Muzny, D. M., Sodergren, E. J., Lu, X., Gibbs, R. A., Homo sapiens Ewing sarcoma breakpoint region 1, transcript variant EWS, mRNA (cDNA clone MGC:5432 IMAGB:3449145), complete cds. BC004817.1 GI:13435962
MGC. Homo sapiens Homo sapiens (human)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (21-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genom
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Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
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Direct Submission
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/db_xref="taxon:9606"
/clone="MGC:5432 IMAGE:3449145"
/clssue_type="Placenta, choriocarcinoma"
/clone_Tib="NIH_MGC_10"
/lab_host="DH10B"
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Homo sapiens (human)
GTCAGCTATACCCAGGCTCAGACCACTGCAACCTATGGGCAGACCGCCTATGCAACTTCT
                                                                                                                 GCACAGACCACCCAGGCATATGGGCAACAAAGCTATGGAACCTATGGACAGCCCACTGAT
                                                                                                                                                           AGCCAAGCTGCAGCGCAGCGGCTACAGTGCTTACACCGCCCAGCCCACTCAAGGATAT
                                                                                                                                                                        AGCCAAGCTGCAGCGCAGCAGGGCTACAGTGCTTACACCGCCCAGCCCACTCAAGGATAT
                                                                                                                                                                                                                  GGACGTTGAGAGAACGAGGAGGAAGGAGAAAATGGCGTCCACGGATTACAGTACCTAT
                                                                                                                                                                                                                              GGACGTTGAGAGAACGAGGAGGAAGGAGAAAATGGCGTCCACGGATTACAGTACCTAT
                                                                                                   GCACAGACCACCCAGGCATATGGGCAACAAAGCTATGGAACCTATGGACAGCCCACTGAT
                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host="JM109"
1. .2189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
/protein_id="CAG30376.1"
/db_xref="GI:47678511"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene="EWSR1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="EWSR1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .2189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone="pGEM.EWSR1"
                                                                                                                                                                                                                                                                                    99.1%;
                                                                                                                                                                                                                                                                      ; Score 2006; D; ; Pred. No. 0; 0; Mismatches
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9; 0;

Length Indels

2189;

3;

Gaps

1

303

183

120 123 60

243 180

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Sanger Institute name: pGEM.EWSR1
Homo sapiens cDNA sequence. This sequence was generated as part of The Wellcome Trust Sanger Institute program to isolate cDNA clones representing the full length open reading frame of well annotated protein coding genes on human chromosome 22. For more information see http://www.sanger.ac.uk/HGP/Chr22/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (Dases 1 to 2189)
Collins, J.E., Wright, C.L., Edwards, C.A., Davis, M.P.,
Cole, C.G., Goward, M.E., Aguado, B., Mallya, M., Mokrab,
Huckle, E.J., Beare, D.M. and Dunham, I.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens EWSR1 full length open reading frame (ORF) cDNA clone (CDNA clone C22ORF:pGEM.EWSR1).
CR456490
CR456490.1 GI:47678510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (24-MAY-2004) Sanger Institute, Hinxton, Cambridge CB10 1SA, UK. E-mail enquiries: c22g@sanger.ac.uk Manuscript
Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cambridgeshire
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,Y.,
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	64 AAAGGCGATGCCACAGTGTCCTATGAAGACCCACCACTGCCAAGGCTGCCGT 	04 AACAAGAGAACTGGGCAACCCATGATCCACATCTACCTGGACAAGGAAACAGGA	4 GACAGTGTGACTCTAGATGATCTGGCAGACTTCTTTAAGCAGTGTGGGGTTGTT	84 CCACCTGTAGATCCAGATGAAGACTCTGACAACAGTGCAATTTATGTACAAGGATT 	24 CGAGGTGGCTTCAATAAGCCTGGTGGACCCATGGATGAAGGACCAGATCTTGATCT	GGAGGCATGAGCAGAGGTGGGCGGGGGAGGAGGACGCGGTGGAATGGGCAGCGCTGG	GAGAACCGGAGCATGAGTGGCCCTGATAACCGGGGCAGGGGAAGAGGGGGATTTGA)TTTATGGGCAGGAGTCTGGAGGATTTTCCGGA 	GCTCCAAGTCAATATAGCCAACAGAGCAGCAGCTACGGGCAGCAGAGTTCATTCCG	AGCAGCTATGGGCAGCAGCCTCCCACTAGTTACCCACCCCAAACTGGATCCTACAG	CAGCAGAACACCTATGGGCAACCGAGCAGCTATGGACA	TACCCTCCTACCAGCTATTCCTCTACACAGCCGACTAGTTATGATCAGAGCAGTII	TACAGTTATCCCCAGGTACCTGGGAGCTACCCCATGCAGCCAGTCACTGCACCTC	CAACCTCAATCTAGCACAGGGGGTTACAACCAGCCCAGC	CAGCCAGCAGCCACTGCACCTACAAGACCGCAGGATGGAAACAAGCCCACTGAGA	GCCTCCTATGCAGCTCAGTCTGCATATGGCACTCAGCCTGCTTATCCAGCCTATG	GTCCAGGGGTATGGCACTGGTGCTTATGATACCACCACTGCTACAGTCA
TGCTCGGAAGAAGCCT 13	CCGTGGAAT	AAGGAAACAGGAAAGCCC 1263 AAGGAAACAGGAAAGCCC 1257	검드넘	ATGTACAAGGATTA ATGTACAAGGATTA	CAGATCTTGATCT CAGATCTTGATCT	GGGCAGCGCTG	검드검	CCGGACCA	CATTCC	CAGO	TCAACAA 7	ACTCT 6		GACAGA GACAGA	CCACTGAG	CAGCCTATO CAGCCTATO	AGTCACCACCACC

	GAGCGCAGAGATCGGCCCTACTAGATGCAGAGACCCCGCAGA 2019	1978	DЬ
	GAGCGCAGAGATCGGCCCTACTAGATGCAGAGACCCCCGCAGA 2025	1984	Ş
TCAG	3 GGAGGAAGAAGAGGACGTGGAGGACCTGGAAAAATGGATAAAGGCGAGCACCGTCAG	1918	뮍
TCAG	GAGGAAGAAGAAGAGGACGTGGAGGACCTGGAAAAATGGATAAAGGCGAGCACCGTCAG	1924	Ş
ATG	TTTGGTGGAGGAAGACGAGGTGGCCCTGGGGGGCCCCTGGACCTTTGATGGAACAGATG	1858	g
- ATG	TTTGGTGGAGGAAGACGAGGTGGCCCTGGGGGGCCCCTGGACCTTTGATGGAACAGATG	1864	Ş
8 8	geregeceregregagacagaegeregerreceregregecegegearegaeegaeegaeege	1798	В
- 8 -	GTGGCCGTGGTGAGACAGAGGTGGCTTCCGTGGTGGCCATGGAGGCAAGATGGACCGGGGCATGGTGGC	1804	Ş
Q.	3 GGCATGCGGGGAAGAAAGAGTGGCCTCATGGATCGTGGTGGTCCCGGTGGAATGTTCAGA	1738	ర్థ
_გ	GCATGCGGGGAGGAAGAGTGGCCTCATGGATCGTGGTGGTCCCGGTGGAATGTTCAGA	1744	Ş
뭐-	gerrecrecececarcerrrececececegergergareareergecagagergereer	1678	рb
_g	GCTTCCTCCGCCACCCTTTCCGCCCCCGGGTGATCGTGATCGTGCAGAGGTGGTCCCTCGT	1684	ð
\$-	GGADACCAGDACTTCGCCTGGAGAACAGAGTGCAACCAGTGTAAGGCCCCADAGCCTGAA	1618	D D
Ξ₿	GGAAACCAGAACTTCGCCTGGAGAACAGAGTGCAACCAGTGTAAGGCCCCCAAAGCCTGAA	1624	Ş
g-	TCTGGAGGAGAAACGTCCAGCACCGAGCTGGAGACTGGCAGTGTCCCAATCCGGGTTGT	1558	망
_년	TCTGGAGGAAGGAAACGTCCAGCACCGAGCTGGAGACTGGCAGTGTCCCCAATCCGGGTTGT	1564	Ś
cc 1557	GTGGAGGAGATAGAGGAGGCTTCCCTCCAAGAGGACCCCGGGGTTCCCCGAGGGAACCCC	1498	탕
_8 _8	CGTGGAGGAGATAGAGGAGGCTTCCCTCCAAGAGGACCCCGGGGTTCCCGAGGGAACCCC	1504	ş
ĠĊ 1497	CTCCGTGGAGGTCCAGGAGGCCCAGGAGGTCCTGGGGGACCCATGGGTCGCATGGGAGGC	1438	ర్జ
_8	CTCCGTGGAGGTCCAGGAGGCCCAGGAG	1444	Ş
CA 1437	CCAATGAACAGTATGCGGGGTGGTCTGCCACCCCGTGAGGGCAGAGGCATGCCACCACCA	1378	뮹
=Ω	CCAATGAACAGTATGCGGGGTGGTCTGCCACCCCGTGAGGGCAGAGGCATGCCACCACCA	1384	Ş

REFERENCE AUTHORS ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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RESULT 8
BC072442
LOCUS
DEFINITION 2164 bp mRNA linear PRI 30-JUN-2004 Homo sapiens Ewing sarcoma breakpoint region 1, transcript variant EWS, mRNA (cDNA clone MGC:87992 IMAGE:6047805), complete cds. BC072442 BC072442.1 GI:48734726 ' Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

El (bases 1 to 2164)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altechul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsleh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S. W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Glbbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

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COMMENT
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Mational Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc.mgc@nlgri.nih.gov
Akhter,N., Ayale,K., Becketrom-Sternberg,S.M., Benjamin,B.,
Akhter,N., Ayale,K., Becketrom-Sternberg,S.M., Haghighi,P.,
Blakesley,R.W., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
McDowell,J., Pearson,R., Stantrippp,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D., Dickson, M.C., Rodriguez, A.C., Grinwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 174 Row: 9 Column: 18
This clone was selected for full length sequencing because it leads to the column of the length sequencing because it length sequen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (01-JUN-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      passed the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol type="maxn"
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SIGYGQSNYSYPQVGSYYMQQFYATAPSYPTSYSSTQPTSYDQSYSQQNTYGQPS
SYGQQSSYGQQSTYPQPTSYPPQTGSYSQAPSQYSQQSSYGQQSSFRQDHDSSMG
VYGQBSGGFGGPGENRSMSGPDNRGRGRGFDRGSMSRGGRGGRGCGWAGAERGCHNKRT
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GQFMJHIYJLNKETGKPKGDATYYSYBDPTAKAAVEMPDGXDFGGFPFRGFRGSRGNP
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/db_xref="MIM:133450"
    SGGGNVQHRAGDWQCPNPGCGNQNFAWRTECNQCKAPKPEGFLPPPFPPPGGDRGRGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="synonym: EWS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      e following selection criteria: matched mRNA gi: 4885224.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'gene="EWSR1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Blakesley,R.W.,
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991 GGAGGACGCGGTGGAATGGGCAGCGCTGGAGAGCGAGGTGGCTTCAATAAGCCTTGGTGGA 1050
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PGGMRGGRGGLMDRGGPGGMFRGGRGGDRGGFRGGRGMDRGGFGGGRRGGPGGPPGPL MEQMGGRRGGRGGPGKMDKGEHRQERRDRPY"

97.7%; Score 1979; DB 9; Length 2164; ity 99.8%; Pred. No. 0; servative 0; Mismatches 0; Indels 3; Gaps	1;
GAGAAAATGGCGTCCACGGATTACAGTACCTATAGCCAAGCTGCAGCGCAGCAGGGCTAC 9	0 0
AGTGCTTACACCGCCCAGCCCACTCAAGGATATGCACAGACCACCCAGGCATATGGGCAA 1	50
CTATGGAACCTATGGACAGCCCACTGATGTCAGCTATACCCAGGCTCAGACCACT 2	10
CCTATGGGCAGACCGCCTATGCAACTTCTTATGGACAGCCTCCCACTGGTTATACT 2	70
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CACTCAGCCTGCTTATCCAGCCTATGGGCAGCAGCAGCAGCAGCCACCTGCACCTACAAGA 45	20
CGCAGGATGGAAACAAGCCCACTGAGACTAGTCAACCTCAATCTAGCACAGGGGGTTAC 5	10
CCCAGCCTAGGATATGGACAGAGTAACTACAGTTATCCCCAGGTACCTGGGAGC 5	70
0 0	30
CAGCCGACTAGTTATGATCAGAGCAGTTACTCTCAGCAGAACACCTATGGGCAACCGAGC 6	90
CTATGGACAGCAGAGTAGCTATGGTCAACAAAGCAGCTATGGGCAGCAGCCTCCCACT 7	20 50
CCACCCCAAACTGGATCCTACAGCCAAGCTCCAAGTCAATATAGCCAACAGAGC 8	10
GCAGCTACGGCAGAGAGTTCATTCCGACAGGACCACCCCAGTAGCATGGGTGTTTAT 87	70
CAGGAGTCTGGAGGATTTTCCGGACCAGGAGAGAACCGGAGCATGAGTGGCCCTGAT 93 	30
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R. Klausher, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.E., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mallahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villaion, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Villaion, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 cione distribution: MGC clone distribution through the I.M.A.G.E. Consortium/LLNL at: Series: IRAK Plate: 12 Row: p Column: 1
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Submitted (25-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                           This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: ang@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Huly:
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzi
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genom Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lou Staudt
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Homo sapiens Ewing sarcoma breakpoint region 1, transcript va
EWS, mRNA (cDNA clone MGC:16900 IMAGE:4340116), complete cds.
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                                                                                                                                                                                                                                                                                                                      clone was selected for full length sequencing at the following selection criteria: matched mR Location/Qualifiers
                                                                                                        /tissue_type="Lymph, lymphoma"
/clone_lib="NIH_MGC_85"
                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MGC:16900 IMAGE:4340116"
                                       note="Vector:
                                                                                                                                                                                                                                                                               organism="Homo sapiens"
                                                                 lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             information can be found http://image.llnl.gov
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Similarity 99.8%;
89; Conservative
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        GCCGACTAGTTATGATCAGAGCAGTTACTCTCAGCAGAACACCTATGGGCAACCGAGCAG
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                                                                                  CCAGCCCAGCCTAGGATATGGACAGAGTAACTACAGTTATCCCCAGGTACCTGGGAGCTA 572
                                                                                                                        GCAGGATGGAAACAAGCCCACTGAGACTGAGTCAATCTAGCACAGGGGGTTACAA
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/db_xref="LocusID:2130"
/db_xref="MIM:133450"
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/codon_start=1
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                                                       CCCACCCACTGCCAAGGCTGCCGTGGAATGGTTTGATGGGAAAGATTTTCAAGGGAGCAA
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This CDS clome is a part of a collection of human full length expression clones generated by BD Biosciences Clontech and the Harvard Institute of Proteomics. Each CDS has been cloned in two forms: with and without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD In-Fusion(TM) cloning system between the Sall and HindIII sites of the pDNR-DUAL vector. Additional sequences in the clone: 'ACC' after Sall site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before HindIII site to maintain reading frame. Clone distribution: http://bioinfo.clontech.com/orfciones.
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Kalnine, N., Chen, X., Rolfs, A., Halleck, A., Hines, L., Eisenstein, S., Koundinya, M., Raphael, J., Moreira, D., Kelley, T., LaBaer, J., Lin, Y., Phelan, M., and Farmer, A.
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(bases 1 to 1971)

Kalnine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein, Kalnine,N., Chen,X., Moreira,D., Kelley,T., LaBaer,J., Lin, Koundinya,M., Raphael,J., Moreira,D., Kelley,T., Labaer,J., Lin, Phelan,M. and Farmer,A.
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Synthetic construct Homo sapiens Ewing sarcoma breakpoint region
mRNA, partial cds.
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                   /product="Homo sapiens Ewing sarcoma breakpoint region
/protein_id="AAP36468.1"
/db_xref="GI:30584431"
                                                                                                                                                                                  /lab_host="DH5alpha T1 resistant"
/note="Vector: pDNR-Dual"
                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:32630"
/clone="GH00297L1.0"
                                                                                                                                       note="Mutations: 1970:Stop->Leu"
                                                                                                                                                                                                                                                                                                                                                  organism="synthetic construct"
translation="MASTDYSTYSQAAAQQGYSAYTAQPTQGYAQTTQAYGQQSYGTY
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Query Match 97.3%; Score 1969.4; DB 12; Length Best Local Similarity 99.9%; Pred. No. 0; Mismatches 1; Indels

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TITLE
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REFERENCE
AUTHORS
TITLE

Unpublished

Oshima,A., Sugiyama,A., Kawakami,B., Nagahari,K., Masuho,Y., Nagai,K. and NEDO human cDNA sequencing project

3 (bases 1 to 2189) Isogai, T., Otsuki, T. and Sugiyama, T Direct Submission

JOURNAL

COMMENT

Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (B-mail:genomics@hri.co.jp, Tel:181-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Blotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key, Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,

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Ono,Y., Hotuta,T., Hiraoka,S., Murakawa,K., Takiguchi,S.,
Kusano,J., Watanabe,M., Fujimori,K., Tanai,H., Ishida,M.,
Yamashita,H., Chiba,Y., Sugiyama,T., Irie,R., Otsuki,T., Sato,H.,
Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y.,
Saito,K., Nishikawa,T., Kimura,K., Watsuo,K., Nakamura,Y.,
Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Takahashi-Fujii,A.,
Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S.,
Magahari,K., Masuho,Y., Nagai,K. and Isogai,T.
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Homo sapiens cDNA FLJ31747 fis, clone NT2RI2007377, highly similar
to RNA-BINDING PROTEIN EWS.
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Mammalia; Eutheria; Primates;
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//db_xref="GI:16551674"

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DRGRGGFGGMGGRGGLMDRGGFGGGMFRGGRGGDRGGFRGGRGMDRGGFGGGRGGPG
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/clone="NT2RI2007377"
/cell_line="NT2"
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/clone lib="NT2RI2"
/clone lib="NT2RI2"
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precursor cells treated 2-weeks mitotic inhibitor after
precursor cells treated ?-weeks mitotic inhibitor after
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                                                                                                                                                                CCACCACTCCGTGGAGGTCCAGGAGGCCCAGGAGGTCCTGGGGGACCCATGGGTCGCATG
                                                                                                                                                                                                                                                                               GAATGGTTTGATGGGAAAGATTTTCAAGGGAGCAAACTTAAAGTCTCCCTTGCTCGGAAG
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                  AACCCCTCTGGAGGAGAAACGTCCAGCACCGAGCTGGAGACTGGCAGTGTCCCAATCCG
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109 CCCACTCAAGGATATGCACAGACCACCCAGGCATATGGGCAACCTAT 168	Query Match 97.0%; Score 1964.4; DB 6; Length 2326; Best Local Similarity 99.9%; Pred. No. 0; Matches 1976; Conservative 0; Mismatches 1; Indels 1; Gaps 1; 49 GATTACAGTACCTATAGCCAAGCTGCAGCGGCAGCAGGGCTACAGTGCTTACACCGCCCAG 108	Patent: WO 02068579-A 16286 06-SEP-2002; PE Corporation (NY) (US) Location/Qualifiers 12326 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"	utheria; Primates; Catarrhini; Hominidae , Adams,M.C., Li,P.W. and Myers,E.W. as nucleic acid arrays, comprising a maj or transcripts, for detecting expression	CQ730352 CQ730352.1 GI:42303963 Homo sapiens (human) Homo sapiens Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, E	78 CGTCA	918 918 978	798 858 858	738 CCTGGTGGCAT 738 CCTGGTGGCAT 738 TTCAGAGGTGG	1618 GGTTGTGGAAACCAGAACTTCGCCTGGAGAACAGAGTGCAAACAGTGTAAGGCCCCAAAG 1677 1678 CCTGAAGGCTTCCTCCCGCCACCCTTTCCGCCCCCGGGTGGTGATCGTGGCAGAGGTGGC 1737	1618 GGTTGTGGAAACCAGAACTTCGCCTGGAGAACAGAGTGCAACCAGTGTAAGGCCCCCAAAG 1677
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                                                                Submitted (20-NOV-2002) Production Sequencing Facility, Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
                                                                                                                                                                                                                                                                                                                                                AC137500 193559 bp DNA linear HTG 20-NOV-2002 Homo sapiens chromosome 16 clone RP11-343G17, WORKING DRAFT SEQUENCE, 2 unordered pieces.
AC137500 AC137500.1 GI:25139894 HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
                                                     Center Cod
Web site:
                                                                                                                                                      2 (bases 1 to 193559)
DOE Joint Genome Institute.
Direct Submission
                                                                                                                                                                                                       Sequencing of Human Chromosome Unpublished
                                                                                                                                                                                                                                             1 (bases 1 to 193559)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                   Project Information
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                                                                                                                                                                                                                                                                                                                               sapiens (human)
Project Name:
                                                    http://www.jgi.doe.gov
                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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FEATURES
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Best Local Similarity
Matches 1949; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Consensus quality: 192718 bases at least Q40
Consensus quality: 192915 bases at least Q30
Consensus quality: 193071 bases at least Q30
Consensus quality: 193071 bases at least Q20
Estimated insert size: 160000; agarose-fp estimation
Estimated insert size: 193459; sum-of-contigs estimation
Quality coverage: 10.21 in Q20 bases; agarose-fp estimation.
Quality coverage: 10.21 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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TACAGITATCCCCAGGTACCTGGGAGCTACCCCATGCAGCCAGTCACTGCACCTCCATCC
                                                                                                                                                                                                                                                                                              GCCTCCTATGCAGCTCAGTCTGCATATGGCACTCAGCCTGCTTATCCAGCCTATGGGCAG
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                                                                             CAGCCAGCAGCACTGCACCTACAAGACCGCAGGATGGAAACAAGCCCACTGAGACTAGT
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                                                                                                                                                                       CAGCCAGTAGCCACTGCACCTACAAGACCGCAGAATGGAAACAAGCCCACTGAGACTAGT
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6 97055; gap of unknown length
6 193559; contig of 96504 bp in length.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /chromosome="16"
/clone="RP11-343G17"
/clone_lib="RPCI human BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . .193559
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Pred. No. 0;
0; Mismatches
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ACTCT ACTC	1624 GGAAACCAGAACTTCGCCTGGAGAACAGAGTGCAACCAGTGTAAGGCCCCAAAGC	1564 TCTGGAGGAGGAAACGTCCAGCACCGAGCTGGAGACTGGCAGTGTCCCAATCCGG	1504 CGTGGAGGAGATAGAGGAGGCTTCCCTCCAAGAGGACCCCCGGGGTTCCCGAGGGAACC	1444 CTCCGTGGAGGTCCAGGAGGCCCAGGAGGTCCTGGGGGACCCATGGGTCGCATGGGAGGC	1384 CCAATGAACAGTATGCGGGGTGGTCTGCCACCCCGTGAGGGCAGAGGCATGCCAC	1324 TITGATGGGAAAGATTITCAAGGGAGCAAACTTAAAGTCTCCCTTGCTCGGAAGAAG 	1264 AAAGGCGATGCCACAGTGTCCTATGAAGACCCACCCACTGCCAAGGCTGCCGTGGAATGG	1204 AACAAGAGAACTGGGCAACCCATGATCCACATCTACCTGGACAAGGAAACAGGAAAG 	1144 GACAGTGTGACTCTAGATGATCTGGCAGACTTCTTTAAGCAGTGTGGGGTTGTTAAGATG	1084 CCACCTGTAGATCCAGATGAAGACTCTGACAACAGTGCAATTTATGTACAAGGATTAAAT	1024 CGAGGTGGCTTCAATAAGCCTGGTGGACCCATGGATGAAGGACCAGATCTTGATCTAGG	964 GEAGGCATGAGCAGAGGTGGGCGGGGAGGAGGACGCGGTGGAATGGGCAGCGCTGG.	904 GAGAACCGGAGCATGAGTGGCCCTGATAACCGGGGCAGGGGAAGAGGGGGATTTGATCGT	844 GACCACCCCAGTAGCATGGGTTTTATGGGCAGGAGTCTGGAGGATTTTCCGGACCAGGA	784 GCTCCAAGTCAATATAGCCAACAGAGCAGCAGCTACGGGCAGCAGAGTTCATTCCGACAG	724 AGCAGCTATGGGCAGCAGCCTCCCACTAGTTACCCACCCCAAACTGGATCCTACAG	664 CAGCAGAACACCTATGGGCAACCGAGCAGCTATGGACAGCAGGAGGAGCTATGGTCAACAA 	JU439 TACCCTCCTACCAGCTATTCCTCTACACAGCCAACTAGTTATGATCAGAGCAGTTACTCT
9 9 9 5 9 5 9 4 9 8 9 2 9 6 9 6 9 6 9 5 9 5 9 6 9 6 9 6 9 6 9 6	CTGAA	GTTGT	8=8	2 1	CACCA 1	경프령	N H	0 0 0	N H	2 1	ი—ი	AGAG 1	ω o	ωφ	ωω	CC # 7	3 7	w

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COMMENT	TITLE	VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS	Db 29 RESULT 14 ACCUS DEFINITION ACCESSION	N N	Qy 16 Db 293 Qy 17 Db 292 Qy 18 Db 292 Qy 18
Submitted (19-DEC-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Feb 28, 2000 this sequence version replaced gi:6692312. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html	Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J. C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Howland, J. C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Handers, T., Leboczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., Norman, C.H., O'Connell, P., Olivar, T.M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Roy, A., Subramanian, A., Talamas, J., Teffaye, S., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Zimmer, A., Direct Submission	ACOLB774.3 GI:7107978 ATGS_PHASE1; HTGS_DRAFT. HTGS_HTGS_PHASE1; HTGS_DRAFT. HOMO sapiens (human) HOMO sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 155815) Birren,B., Linton,L., Nusbaum,C., and Lander,E. Homo sapiens, clone RP11-20G3 Unpublished 2 (bases 1 to 155815) Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,	1984 GAGCGCAGAGATCGGCCCTACTAGATGCAGAGACCCCGCAGA 2025	O TTTGGTGGAGGAAGACAAGGTGGCCCTGGGGGGGCCCCC-GGACCTTTGATGTAACCAATG GGAGGAAGAAGAAGAAGACGTGGAGGACCTTGAAAAAAATGGATAAAAGGCGAGCACCGTCAG	8 7 4 V C C A

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Best Local Similarity
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10654
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                                                                                                                                                                                                                                                           10474 GCACAGACCACCCAGGCATATGGGCAACAAAGCTATGGAACCTATGGACAGCCCATTGAT 10533
                                          304
                                                                                                                                                                                               184 GTCAGCTATACCCAGGCTCAGACCACTGCAACCTATGGGCAGACCGCCTATGCAACTTCT 243
                                                                                                          124
                                                                                                                                                                                                                                                                                                                                                                          64 AGCCAAGCTGCAGCGCAGCAGGGCTACAGTGCTTACACCGCCCAGCCCACTCAAGGATAT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 GGACGTTGAGAGAACGAGGAGGAGGAGAAAATGGCGTCCACGGATTACAGTACCTAT 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center project name: L3897
Center clone name: 20 G 3
Sequencing vector: M13; M77815; 100% of reads chemistry: Dye-terminator Big Dye; 100% of read Assembly program: Phrasp; version 0.960731
Consensus quality: 150190 bases at least Q40
Consensus quality: 153018 bases at least Q30
Consensus quality: 153018 bases at least Q20
Insert size: 155015; sum-of-contigs
Insert size: 155615; sum-of-contigs
                                                                                    GCACAGACCACCCAGGCATATGGGCAACAAAGCTATGGAACCTATGGACAGCCCACTGAT 183
                        GTCCAGGGGTATGGCACTGGTTATGATACCACCACTGCTACAGTCACCACCACCAG 10713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92.8%; Score 1879.6; larity 96.2%; Pred. No. 0; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="texon:9606"
/clone="RPP1-2063"
/clone lib="RPCI-11 Human M
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6153. .23133
/note="assembly_fragment
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clone_end:T7
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3 6152; gap of 100 bp
3 2313: contig of 1981 bp in length
4 23233: gap of 100 bp
4 155815: contig of 132582 bp in length.
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ACAGTATGCAGGGTGGTATGCCACCCCATGAGGGCAGAGGGATGCCACCC	CAGTATGC	11734	망
ACAGTATGCGGGGTGGTCTGCCACCCGTGAGGGCAGAGGCATGCCACCA 14	TGAACAGTATGC	38	Ş
HARAGATTTTCAAGGGAGCAAACTTAAAGTCTCTCTTGCTCGGAAGAGG	TTTGATGGGAAAGATTTTCAAGG	6	망
SGAAAGATTTTCAAGGGAGCAAACTTAAAGTCTCCCTTGCTCGGAAGAAGCCT 1	GAAAGATTT	1324	Ş
TGTGAAGACTCACCTACTGCCAAAGCTGCCGTGGAATGG 1	AAAGGTGATGCCACAGTGTCCTG	6	gg
ATGCCACAGTGTCCTATGAAGACCCACCCACTGCCAAGGCTGCCGTGGAATGG 1323	CGATGCCACAGTGT	N	Ş
CCATGATCCACACCTACCTGGACAAGGAAACAAGAAAGCC	വ–		뮍
GAACTGGGCAACCCATGATCCACATCTACCTGGACAAGGAAACAGGAAAGCCC 1263	ACAAGAGAACTGGGCAACC	N	Ş
FIGACTCTAGATGATCTGGTAGACTTCTTTAAGCAGTGTGGGGGTTGTTAAGATG 11553	8=	11494	밁
AGTGTGACTCTAGATGATCTGGCAGACTTCTTTAAGCAGTGTGGGGGTTGTTAAGATG 1203	GACAGTGTGACTCTAGATGATCT	1144	β
TAAA	CCACCTGTAGATCCAGATGAAGA	11434	뮍
AGATCCAGATGAAGACTCTGACAACAGTGCAAT	CACCIGI	1084	S
CTTCAATAAGCCTGGTGGACCCATGGATGAAGGACCAGATCTTGATCTAGG	ξ=	11374	ర్జ
CTTCAATAAGCCTGGTGGACCCATGGATGAAGG	GGCTTCAA	1024	Ş
ହ=	GGAGGCATGAGCAGAGGTGGGCG	11314	타
CATGAGCAGAGGTGGGCGGGGAGGACGCGCGGTGGAATGGGCAGCGCTGGAGAG 1023	-63	964	Ś
CATGAGTGGCCCTGATAACTGGGGCAGGGGAAGAGGGGGGATTTGAT	GAGAACCGGAGCATGAGTGGCCC	11254	뮍
GGAGCATGAGTGGCCCTGATAACCGGGGCAGGGGGAAGAGGGGGGATTTGATCGT 963	CCGGA	. 904	Ş
CAGGAGTCTGGAGGATTTTCCGGAC	GACCACCCCAGTAGCATGGGTGT	11194	뫄
CCAGTAGCATGGGTGTTTATGGGCAGGAGTCTGGAGGATTTTCCGGACCAGGA 903	GACCACCCCAGTAGCATGGGTGTTTATGGG	844	Ş
AGCTACGGGCAGCAGAGTTCATTCTC	GCTCCAAGTCAGTATAGCTAACAC	11134	DЪ
CCAACAGAGCAGCAGCTACGGGCAGAGCTTCATTCCGACA	CCAAGTCAATATAGCCA	784	Q
TGCCTCCCACTAGTTACCCACCCCAAACTTGA	AGCAGCTATGGGCAGCTGCCTCCC	11074	ర్జ
ATGGGCAGCAGCCTCCCACTAGTTACCCCACCCAAACTGGATCCTACAGCCAA 783	GCAGCTATGGGCAG	724	Ş
CACCTATGGGAAACCGAGCAGCTATGGACAGCAGAGTAGCTATGGTCAA	CAGCAGAACACCTATGGGAAACCC	11014	탕
ACACCTATGGGCAACCGAGCAGCTATGGACAGCAGAGTAGCTATGGTCAACAA 723	CAGAA	664	Ş
CTACCAGCTATTCCTCTACACAGCCAACTAGTTATGATCAGAGCAGTTACT	TACCCTCCTACCAGCTATTCCTCT	10954	ర్జ
TIACCAGCTATTCCTCTACACAGCCGACTAGTTATGATCAGAGCAG	ACCCTCCTACCA	604	Ś
TCCCCAGGTACCTGGGAGCTACTCCATGCAGCCAGTCACCGCACCTCCATC	TATCC	10894	D _P
ATCCCCAGGTACCTGGGAGCTACCCCATGCAGCCAGTCACTGCACCTCCATCC 603	CAGTTATCC	544	Ś
CTAGCACAGGGGTTACAACCAGCCCAGCCTAGGATATGGACAGAGTAA	CAACCTCAATCTAGCACAGGGGGT	10834	벍
AATCTAGCACAGGGGGTTACAACCAGCCCAGCCTAGGATATGGACAGAGTAAC 543	CCTCAATCTAG	484	Ş
AGCCACTGCACCTACAAGACTGCAGAATGGAAACAAGCCCACTGAGACTA	CAGCCAGTAGCCACTGCACCTACA	74	ఠ
GCCACTGCACCTACAAGACCGCAGGATGGAAACAAGCCCCACTGAGACTAG	-ถ	24	Ş
TCAATCTGCATATGGCACTCAGCCTGCTTATCCAGCTTATGGGC	GCCTCCTATGCAGCTCAATCTGCA	14	당
ATGCAGCTCAGTCTGCATATGGCACTCAGCCTTATCCAGCCTATGGGCAG 423	GCCTCCTATGCAGCTCAGTCTGCA	64	Ą

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AUTHORS
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L Submitted (10-MAR-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Mar 11, 2002 this sequence version replaced gi:15944185. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 10), an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11914
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 180718)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGCATGTGGGGAAGAGGTGGCCTCATGGATCATGGTGGTCCCGGTGGAATGTTCAGA
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om clone RP11-9L18 on chromosome 1, complete
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          GCCTCCTATGCAGCTCAATCTGCATATGGCACTCAGCCTGCTTATCCAGCTTATGGGCAG 157206
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence is the entire insert of clone RP11-9118 The true left end of clone RP11-479J7 is at 136234 in this sequence. The true right end of clone RP11-375H19 is at 73742 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISSPROT: Tr:, TREMBL; Wp:, WORMPEP; Information database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VECTOR: pBACe3.6
GCCTCCTATGCAGCTCAGTCTGCATATGGCACTCAGCCTGCTTATCCAGCCTATGGGCAG
                                                                                                                    GTCCAGGGGTATGGCACTGGTGCTTATGATACCACCACTGCTACAGTCACCACCACCACCAG
                                                                                                                                                                                                 AGCCAAGCTGCAGCGCAGCAGGGCTACAGTGCTTACACCGCCCAGCCCACTCAAGGATAT 123
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                                                                                  GTCCAGGGGTATGGCACTGGTGCTTATGATACCACCACTGCTACAGTCACCACCACCCAG
                                                                                                                                                                                                                                                                                                                      GTCAGCTATACCCAGGCTCAGACCACTGCAATCTATGGGCAGACCGCCTATGCAACTTCT 157386
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/note="[] Unsure [x] Misc_feature Then select the text
for the note(s) - [] Tandem repeat [] Single clone
region [] Forced join [x] Other Add a comment here -
Sequence from AC011221 and AC018774 sequenced by WIBR."

complement (46397. .46442)

/note="Single clone region. Sequence from reads from a
short insert library derived from a single pUC clone.
Restriction digest data confirm the assembly."

complement (102116. .102124)

/note="767 bases of IS1 transposon (X52534) removed here.
This sequence represents the duplicated flanking sequence
of the IS1."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Sequence confirmed sequenced by WIBR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="RPCI-11.1"
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/mol_type="genomic DNA"
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	1503 156126	1444 CTCCGTGGAGGTCCAGGAGGCCCAGGAGGTCCTGGGGGACCCATGGGTCGCATGGGAGGC 151	Qy 1: Db 156:	
	56186	84 CCAATGAACAGTATGCGGGGTGGTCTGCCACCCCGTGAGGGCAGAGGGCATGCCACCA 1	Qy 13 Db 1562	
	383 56246	1324 TITGATGGGAAAGATTTTCAAGGGAGCAAACTTAAAGTCTCCCTTGCTCGGAAGAAGCCT 1383 	Oy 1:	
	1323 156306	1264 ANAGGCGATGCCACAGTGTCCTATGAAGACCCACCCACTGCCAAGGCTGCCGTGGAATGG 1323 	Qy 1: Db 156:	
	1263 156366	1204 AACAAGAGAACTGGGCAACCCATGATCCACATCTACCTGGACAAGGAAAACAGGAAAGCCC 1263 	Qy · 1:	
	1203 156426	1144 GACAGTGTGACTCTAGATGATCTGGCAGACTTCTTTAAGCAGTGTGGGGGTTGTTAAGATG 1203 	Qy 1: Db 156	
	1143 156486	1084 CCACCTGTAGATCCAGATGAAGACTCTGACAACAGTGCAATTTATGTACAAGGATTAAAT 1143 	Qy 10 Db 1569	
	1083 156546	1024 CGAGGTGGCTTCAATAAGCCTGGTGGACCCATGGATGAAGGACCAGATCTTGATCTAGGC 1083	Oy 10 Db 156	
	1023 156606	964 GGAGGCATGAGCAGAGGTGGGCGGGGAGGAGGACGCGGTGGAATGGGCAGCGCTGGAGAG 1023 	Oy :	
	963 156666	904 GAGAACCGGAGCATGAGTGGCCCTGATAACCGGGGCAGGGGAAGAGGGGGATTTGATCGT 963 	Оу :	
	903 156726	844 GACCACCCCAGTAGCATGGGTGTTTATGGGCAGGAGTCTGGAGGATTTTCCGGACCAGGA 903 	Qy	~ ~
	843 156786	784 GCTCCAAGTCAATATAGCCAACAGAGCAGCAGCAGCAGCAGCAGAGTTCATTCCGACAG 843 	Qу .	
	783 156846	724 AGCAGCTATGGGCAGCAGCCTCCCACTAGTTACCCACCCCAAACTGGATCCTACAGCCAA 783 	Оу . Db 156	
	6906	664 CAGCAGAACACCTATGGGCAACCGAGCAGCTATGGACAGCAGAGTAGCTATGGTCAACAA 723	Qy (
	6966	604 TACCCTCCTACCAGCTATTCCTCTACACAGCCGACTAGTTATGATCAGAGCAGTTACTCT 663	Qy (
	603 157026	544 TACAGTTATCCCCAGGTÁCCTGGGAGCTACCCCATGCAGCCAGTCACTGCACCTCCATCC 603	Qy ! Db 157	
_	7086	484 CAACCTCAATCTAGCACAGGGGGTTACAACCAGCCCAGC	Qy , рь 157:	
	483 157146	424 CAGCCAGCAGCCACTGCACCTACAAGACCGCAGGATGGAAACAAGCCCACTGAGACTAGT 483	Qy ,	
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	17 GAGCGCAGAGATCAGCCCTACTAGATGCAGAGAACCCGCAGA 155606	155647	닭
	94 GAGCGCAGAGATCGGCCCTACTAGATGCAGAGACCCCCGCAGA 2025	1984	Ş
155648	GGAGGAAGAAGAGGACGTGAAGGACCTGGAAAAAACGGATAAAGGCGAGCACTGTCAG	155707	
1983	GAGGAAGAAGAGGAGGACGTGGAGGACCTGGAAAAATGGATAAAGGCGAGCACCGTCAG	1924	Ş
155708	TTTGGTGGAGGAAGACAAGGTGGCCCTGGGGGGCCCCC-GGACCTTTGATGTAACCAATG	155766	뮍
1923	TTTGGTGGAGGAAGACGAGGTGGCCCTGGGGGGCCCCCTGGACCTTTTGATGGAACAGATG	1864	Ş
155767	GGTGGCTGTGGTAGAGACAGAAGTGGCTTCTGTGGTGG-CTGGGCATGGACCGAGGTGGC	155825	문
1863	GGTGGCCGTGGTGGAGACAGAGGTGGCTTCCGTGGTGGCCGGGCATGGACCGAGGTGGC	1804	Ş
155826	GGCATGTGGGGAGGAAGAGGTGGCCTCATGGATCATGGTGGTCCCCGGTGGAATGTTCAGA	155885	뮍
1803	GGCATGCGGGGAAGGAAGAGTGGCCTCATGGATCGTGGTGGTCCCGGTGGAATGTTCAGA	1744	ş
155886	GGCTTCCTCCCGCCTTCCCACCCTCCGGGTGGTGATCATGGCAGAGGTGGCCCTGGT	155945	ᅡ
1743	GGCTTCCTCCCGCCACCCTTTCCGCCCCCGGGTGGTGATCGTGGCAGAGGTGGCCCTGGT	1684	ð
155946	GGAAACCAGAACTTCGCCTGGAGAACAGAGAGCAACAAGTGTAAGGCTCCAAAGCCTGAA	156005	
1683	GGAAACCAGAACTTCGCCTGGAGAACAGAGTGCAACCAGTGTAAGGCCCCAAAGCCTGAA	1624	δ
156006	TCTGGAGGAGGAAACGTCCAGCACCAAGCTGGAGACAGGCAGTGTCCCCAATCCGGGTTGT	156065	F
1623	TCTGGAGGAGGAAACGTCCAGCACCGAGCTGGGAGACTGGCAGTGTCCCAATCCGGGTTGT	1564	Ş
156066	CGTGGAGGAGATAGAGGACCTCCCTCCAAGAGGACCCCAGGGTTCCCGAGGGAACACC	156125	닭
1563	CGTGGAGGAGATAGAGGAGGCTTCCCTCCAAGAGGACCCCCGGGGTTCCCCGAGGGAACCCCC	1504	Š.

Search completed: February 20, 2005, 11:50:27 Job time: 8507.87 secs

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Result
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    Pred. No. 18 the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Aas70647 DNA encod
Acn37537 Tumour-as
Aas62623 CDNA sequ
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Ada53506 Human cod
Adr07446 Full leng
Adp56333 Human PRO
Aag50646 Human Ews
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19.7	20.3	20.3	20.3	20.3	20.3	20.3	20.3	20.3	20.7	20.9	23.7	24.1	25.1	25.4	25.4	25.4	25.4	25.4	25.4	25.4	25.4	28.1	32.3	34.9
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Ach16656 Human adu	Human	Abs35546 Human liv	Aak09942 Human bra	Aak35836 Human bon	Aba29300 Probe #77		Aba61641 Human foe	Aai17153 Probe #70	Aav86051 EST clone	Aac01659 Human sec	Ach22345 Human adu	Acn37539 Tumour-as	Ach40478 Human foe	Abs10394 Human gen	Abs36007 Human liv	Aak10423 Human bra	Aak36327 Human bon	Aba29535 Probe #80	Aai42050 Probe #10	Aba62106 Human foe	Aai17281 Probe #72	Acn88697 Breast ca	Aal26725 Human bre	Acn37538 Tumour-as

Human tumour-associated antigenic target (TAT) cDNA sequence #2904. ADQ86032; ADQ86032 standard; cDNA; 2372 22-JUL-2004. WO2004060270-A2 Homo sapiens. human; tumour-associated antigenic target; TAT; cytostatic; gene therapy; cancer; cell proliferative disorder; gene; ss. 07-OCT-2004 (first entry) BP.

ALIGNMENTS

The present invention describes an isolated tumour-associated antigenic target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of (a); (c) the complement of (a) or (b); (d) a sequence that has 80% sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-(c). Also described: (1) an expression vector comprising the above

nucleic acid; (2) a host cell comprising the above expression vector; (3)

New nucleic acid molecule and encoded polypeptide, f preventing or treating cell proliferative disorders

for diagnosing, s such as cancer.

Claim 1; SEQ ID NO 2904; 5504pp; English.

Wu TD,

Zhou Y;

(GETH) GENENTECH INC. (WUTD/) WU T D. (ZHOU/) ZHOU Y.

18-OCT-2002; 2002US-0418988P 15-OCT-2003; 2003WO-US029126

WPI; 2004-534300/51.

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cc comprising: (a) an amino acid sequence encoded by any of the above nucleotide sequences; (b) an amino acid sequence encoded by the full-cc length coding region of the above nucleotide sequences; or (c) a sequence cc chaving at least 80% identical to (a) or (b); (5) a chimeric polypeptide; (6) can isolated antibody that binds to the above polypeptide; (7) a process cf or producing the antibody; (8) an isolated oligopeptide that binds to the above polypeptide; (7) a process cf binding organic molecule that binds to the above polypeptide; (10) a composition of matter comprising the above (chimeric) polypeptide; (10) a composition of matter comprising the above (chimeric) polypeptide; (10) a composition of matter contained within the container; (12) methods of inhibiting the growth of a cell that expresses the above portein, where the growth of the cell is at least in part dependent upon a growth cells that express the above protein; (13) a method of the respectation of a protein in a sample suspected of containing the presence of a protein in a sample suspected of containing the protein; (14) a method of described above; (15) methods of diagnosing the presence of a tumour in a sample suspected of containing the protein cannot composited with increased expression or activity of the above protein; and (17) a method of diagnosing the presence of a tumour in a sample suspected of containing the protein cannot composited with increased expression or activity of the above contain; and (17) a method of binding an antibody, oligopeptide or composition and methods are useful for diagnosing, gene containing or treating cancer. The composition is also used for preparing a medicament for the therapeutic treatment or diagnosing, gene call proliferative disorder or cancer. The present sequence represents a contain of the composition of the composition of the composition of the composition can
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25-APR-2003; 2003US-0465692P.
                                                                                               Determining the hormonal effects of substances, used to identify pharmaceuticals, e.g. for treatment of androgen receptor dysfunction, from modulating interaction between nuclear receptors and Ewing sarce
                                                                                                                                                                                                                                                                                                                                                                           16-FEB-2004; 2004EP-00003422
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hypogonadism; and
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This invention relates

to a novel modulators that alter the interaction

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CAAAGCAGCTATGGGCAGCAGCCTCCCACTAGTTACCCCACCCCAAACTGGATCCTACAGC

TCTCAGCAGAACACCTATGGGCAACCGAGCAGCTATGGACAGCAGAGTAGCTATGGTCAA

TCTCAGCAGAACACCTATGGGCAACCGAGCAGCTATGGACAGCAGAGTAGCTATGGTCAA

TCCTACCCTACCAGCTATTCCTCTACACAGCCGACTAGTTATGATCAGAGCAGTTAC

TCCTACCCTCCTACCAGCTATTCCTCTACACAGCCGACTAGTTATGATCAGAGCAGTTAC

AACTACAGTTATCCCCAGGTACCTGGGAGCTACCCCATGCAGCCAGTCACTGCACCTCCA

AACTACAGTTATCCCCAGGTACCTGGGAGCTACCCCATGCAGCCAGTCACTGCACCTCCA

CAGCAGCCAGCAGCCACCTACAAGACCGCAGGATGGAAACAAGCCCACTGAGACT CAGCAGCCAGCAGCCACCTGCACCTACAAGACCGCAGGATGGAAACAAGCCCCACTGAGACT CAGGCCTCCTATGCAGCTCAGTCTGCATATGGCACTCAGCCTGCTTATCCAGCCTATGGG CAGGCCTCCTATGCAGCTCAGTCTGCATATGGCACTCAGCCTGCTTATCCAGCCTATGGG CCTGTCCAGGGGTATGGCACTGGTGCTTATGATACCACCACTGCTACAGTCACCACCACC

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CC between the Ewing sarcoma protein (EWS) and its nuclear receptor, as well CC as the screening method thereof. Specifically, it refers to determining CC and identifying a hormonal effect brought about by test compounds that CC modulate either the binding of EWS to the nuclear receptor or the ligand-CC nuclear receptors as including osestrogen, progesterone, thyroid hormone, CC vitamin D, and retinoic acid receptors, most preferably they are androgen CC receptors. Accordingly, these modulators may be used in the development CC of pharmaceutical compositions that can diagnose and be used to treat CC diseases associated with receptor dysfunction such as prostatic cancer, CC alopecia, acne, hypogonadism and androgen-resistance syndrome e.g. CC testicular feminisation. This method provides reliable, sensitive, CC simple, inexpensive and rapid assessment of the hormonal effects of these CC test compounds. This polynucleotide sequence is the cDNA encoding the Naman Ewing sarcoma protein of the invention.
Sequence 2390 BP; 646 A; 589 C; 668 G; 487
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100.0%; Score 2025; 100.0%; Pred. No. 0;

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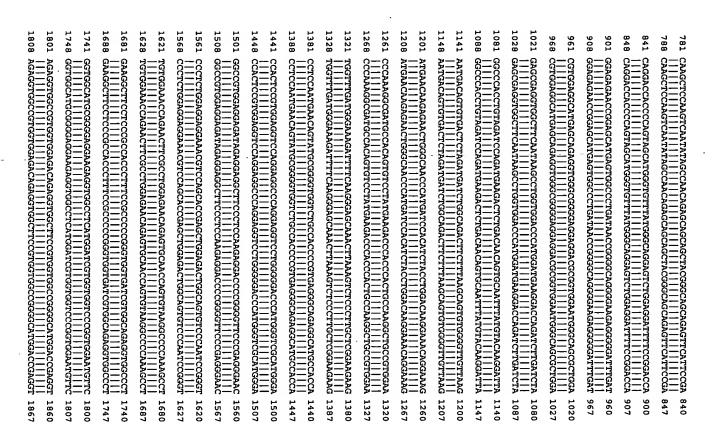
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301 248 241 188 181 128 121 8 61 œ CCTGTCCAGGGGTATGGCACTGGTGCTTATGATACCACCACTGCTACAGTCACCACCACC TCTTATGGACAGCCTCCCACTGGTTATACTACTCCAACTGCCCCCCAGGCATACAGCCAG GATGTCAGCTATACCCCAGGCTCAGACCACTGCAACCTATGGGCAGACCGCCTATGCAACT TATGCACAGACCACCCAGGCATATGGGCAACAAAGCTATGGAACCTATGGACAGCCCACT TATGCACAGACCCACCCAGGCATATGGGCAACAAAGCTATGGAACCTATGGACAGCCCACT TATAGCCAAGCTGCAGCGCAGCAGGCTACAGTGCTTACACCGCCCAGCCCACTCAAGGA TATAGCCAAGCTGCAGCGCAGCAGGGCTACAGTGCTTACACCGCCCAGCCCACTCAAGGA GACGGACGTTGAGAGAACGAGGAGGAGGAGAGAAAATGGCGTCCACGGATTACAGTACC TCTTATGGACAGCCTCCCACTGGTTATACTACTCCAACTGCCCCCCAGGCATACAGCCAG GATGTCAGCTATACCCAGGCTCAGACCACTGCAACCTATGGGCAGACCGCCTATGCAACT GACGGACGTTGAGAGAACGAGGAAGGAAGGAGAAAATGGCGTCCACGGATTACAGTACC Conservative <u>,</u> Mismatches 0. Indels 0 360 127 120 67 307 300 247 240 187 180 0

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WO200228999-A2

11-APR-2002.

03-OCT-2001; 2001WO-US030821

03-OCT-2000; 2000US-0237189P

(GENE-) GENE LOGIC INC

Beazer-Barclay Y, Weissman SM, Yamaga ູເດ Ç

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Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and drug toxicity.

Claim 1; SEQ ID NO 1199; 114pp; English.

CGCA), by detecting the level of expression of gene(s) (GS) identified by CDNA chip analysis as given in the specification, and comparing the CC expression level to an expression level in an unactivated GC, where CC differential expression of GS is indicative of GCA. Also included are CC expression of at least one gene in GS; (2) screening (M3) for an agent capable of modulating GCA or an inflammation (especially chronic) in a CC tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the gene expression CC pathogen or sterile inflammatory disease using the gene expression a CC pathogen or sterile inflammatory disease, by detecting the level of cexpression in a sample of the tissue of gene(s) from GS, where the level of expression in a sample of the tissue of sinflammation; (4) treating CC (M5) an inflammator (especially chronic) or in a tissue, an allergic response in a subject to a pathogen or sterile inflammation (especially chronic) or in a tissue, an allergic cresponse in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by contacting a tissue having inflammation with an confident of the tissue confident of the tissue having inflammation with an agent that modulates the expression of gene(s) from GS in the tissue. M1 invention relates to detecting (M1) granulocyte (GC) activation

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CC inflammation in a tissue; M4 is useful for detecting an inflammation; contains a tissue; M4 is useful for detecting an inflammation; cc especially chronic) in a tissue, an allergic response in a subject; consolidation of a subject to a pathogen or sterile inflammatory disease (e.g. psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal reperfusion injury, ARDS, adult conspiratory distress syndrome, inflammatory bowel disease, Crohn's confiction, useful for treating one of the infection, protozoal infection, parasitic infection, protozoal infection, parasitic infection, protozoal infection, parasitic infection, protozoal infection, protozo
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The invention relates to a method of diagnosing (I) the onset or comparession of benign prostatic hyperplasia (BPH), or screening (II) for or identifying an agent that modulates the onset or progression of BPH. Can be the control of the method is based on changes in gene expression in BPH tissue isolated from patients exhibiting different clinical states of prostate control of the subject that are differentially regulated compared to normal prostate tissue. (I) comprises confidently prostate cells (II) comprises preparing a first gene expression profile of BPH cells or BPH-like cell population, exposing the cells to the cells, preparing a second gene expression profile of the agent exposed cells, and comparing the first and second gene expression profiles. (I) contified in a rissue or cells, by comparing the onset or progression of BPH. (II) is useful for identifying an agent that modulates the onset or progression of BPH. (Cells at issue or cells, by comparing the expression level of genes confident in the tissue or cells to the level of expression of gene in the database, and displaying the expression levels of at least one gene in the database, and displaying the expression levels of the level of prostate cancer. ABK64106-ABK64860 represent human benign prostatic constatic hyperplasia gene sequences of the invention
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13-AUG-2002 ABN97274 standard; DNA; 2390 (first entry) BP.

#3772 used to diagnose liver cancer.

Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic; metastatic liver tumour; cytostatic; expression profile; disease st disease progression; drug toxicity; drug efficacy; drug metabolism.

11-APR-2002

02-OCT-2001; 2001WO-US030589

02-OCT-2000; 2000US-0237054P

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(GENE-) GENE LOGIC INC.

Horne Alvares C, Peres-Da-Silva Ś Vockley

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Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a patient, involves detecting the level of expression of two or more genes in a liver tissue sample.

Claim 1; SEQ ID NO 3772; 298pp; English.

The invention relates to a novel method for diagnosing and detecting the CC progression of liver cancer, hepatocellular carcinoma or metastatic liver cumour in a patient, and differentiating metastatic liver cancer from CC hepatocellular carcinoma in a patient, involving detecting the level of expression of two or more genes represented in ARN93503-ARN97455 in a CC tissue sample. The method of the invention has hepatotropic, and CC tycostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic CC liver carcinoma in a patient. The method is useful for identifying CC expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, CC drug toxicity, drug efficacy and drug metabolism. Note: The sequence data CC obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 2390 BP; 645 A; 589 C; 668 G; 488 T; 0 U; 0 Other;

5 S ঠ 밁 밁 밁 Ś Query Match Best Local Simi Matches 2024; Local Similarity 181 128 121 89 61 GATGTCAGCTATACCCAGGCTCAGACCACTGCAACCTATGGGCAGACCGCCTATGCAACT TATGCACAGACCCACCCAGGCATATGGGCAACAAAGCTATGGAACCTATGGACAGCCCACT TATAGCCAAGCTGCAGCGCAGCAGGGCTACAGTGCTTACACCGCCCAGCCCACTCAAGGA GACGGACGTTGAGAGAACGAGGAGGAGGAGAGAAAATGGCGTCCACGGATTACAGTACC GACGGACGTTGAGAGAACGAGGAGGAAGGAGAAAATGGCGTCCACGGATTACAGTACC Conservative 99.9%; Score 2023.4; 100.0%; Pred. No. 0; 0, Mismatches BB 1: 6, Indels Length 2390; 0, 240 180 187 67

RESULT 5
ABN97274

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standard; CDNA; 2390 ₽₽

18-NOV-2004 (first entry)

Tumour-associated antigenic target (TAT) CDNA DNA269830, SEQ ID NO:5989.

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X Tumour-associated antigenic target; TAT; human; overexpression; c tumour; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoma; leukaemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping; therapy; cytostatic; gene; cancer;

WO2004030615 ÷ A2

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15-APR-2004.

29-SEP-2003; 2003WO-US028547

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The invention relates to human tumour-associated antigenic target (TAT) CC polypeptides, and their related nucleic acids. The TAT polypeptides are CC overexpressed in cancer tissues compared to normal tissues, and may thus conversely the invention also relates to nucleic acid and polypeptide serve as effective targets for the diagnosis and treatment of cancer in CC mammals. The invention also relates to nucleic acid and polypeptide sequences at least 80% identical to the TAT nucleic acids and cards and cards; an antibody specific for a TAT polypeptide; apeptide or organic cmolecule which binds to a TAT polypeptide; fusion proteins comprising a CC molecule which binds to a TAT polypeptide; fusion proteins comprising a CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder cancer, pancreatic cancer, cervical cancer, cancers of the central nervous system, melanoma and leukaemia. TAT nucleic acids may further be cused as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid of EWS gene and its hybrid(s) - contg. gene sequence involved in chromosomal trans-location, also derived mRNA, probes, fusion proteins etc., for diagnosis and treatment of Ewing sarcoma and melanoma.
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New polynucleotides encoding secreted asthma, HIV and Crohn's disease. proteins useful for treating ø

WPI; 2002-010900/01

06-APR-2000; 2000US-0195604P 29-MAR-2001; 2001WO-US010485

GENETICS INST INC

Clark HF, K, Graham

Fechtel JR;

ζ,

Agostino MJ,

Howes

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Resnick

RJ;

18-OCT-2001.

1; Page 100; 391pp; English.

The present invention relates to the isolation of novel cDNA sequences which encode human secreted proteins. The cDNA sequences have been derived from a variety of human tissues. The invention also provides a method for producing proteins from these polymuclaotide sequences. The compounds that modulate expression of the polymuclaotide sequences of activity and production, and the cell is also useful for identifying compounds that modulate expression of the polymuclaotide sequences compounds that modulate expression of the polymuclaotide sequences of treating diseases such as hyperproliferative disorders (e.g. cancer), fimune deficiency disorders (e.g. severe combined immunodeficiency (SCID)), autoimmune disorders (e.g. severe combined immunodeficiency (SCID)), autoimmune disorders (e.g. multiple sclerosis), blood disorders (e.g. thrombocytopaenia), inflammatory disorders (e.g. arthritis) and confectious disorders (e.g. hepartitis). The polymuclaotide sequences of the invention are also useful in gene therapy. AAS62214-AAS62838 proteins

2176 BP; 413 ₽ 617 Ç 563 G; 583 Ŧ; 0 ς. 0 Other;

Query Match Best Local Similarity Matches 1998; Conserv Conservative 98.1%; 99.9%; ; Score 1986.4; Pred. No. 0; O; Mismatches DB 1; 9 Indels Length 2176; 1; Gaps

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986 GGGANGAGGACGCCGGTGGAATGGCCAGCCTGGAGAGCGAGAGCTGCTCAATAAGCCTG 1045	AAGGAGAGAAAATGGCGTCCACGGATTACAGTACCTATAGCCAAGCTGCAGGCAG
RESULT 1 AAS7064 XX XX AC AC AC AC XX XX AC	\$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$
ILT 9 10647 AAS70647 standard; cDNA; 2388 BP. AAS70647; 13-FEB-2002 (first entry) DNA encoding novel human diagnostic protein #6451.	116 TOGGCAACTTCTTTTAACCAGTTGTTTACAACTGATTAAATGATCAACAGAAAACTTCAAATGATTCAACTCAAATGATTAAATGATTAAATGATTAAATGAAATGATTAAATGAATGATTCAAATGATTAAATGATTAAATGAAATGATTAAATGAATG

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                                                                                                                                                                                                                                                                                                       The invention relates to isolated polynucleotide (I) and polypeptide (II)
C sequences. (I) is useful as hybridisation probes, polymerase chain
C reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
C and in recombinant production of (II). The polynucleotides are also used
C in diagnostics as expressed sequence tags for identifying expressed
C genes. (I) is useful in gene therapy techniques to restore normal
C useful for generating antibodies against it, detecting or quantitating a
C useful for generating antibodies against it, detecting or quantitating a
C upplement. (II) and its binding partners are useful in medical imaging
C supplement. (II) and its binding partners are useful in medical imaging
C supplement protein expression or biological activity. The
C involving aberrant protein expression or biological activity. The
C diagnostics, forensics, gene mapping, identification of mutations
C responsible for genetic disorders or other traits to assess biodiversity

The polymeration of mutations
C responsible for genetic disorders or other traits to assess biodiversity
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Matches 2015
                                                                                                                                                                                                                                                                                                                                             and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                       Sequence
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mes 2015; Conserv
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The invention relates to human tumour-associated antigenic target (TAT) cc polypeptides, and their related nucleic acids. The TAT polypeptides are coverexpressed in cancer tissues compared to normal tissues, and may thus gerve as effective targets for the diagnosis and treatment of cancer in cc mammals. The invention also relates to nucleic acid and polypeptide compared to the TAT nucleic acids and treatment of cancer in cc acid; an antibody specific for a TAT polypeptide; a peptide or organic complexity an antibody specific for a TAT polypeptide; a peptide or organic complexity and methods and compositions for the treatment or cc diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, and compositions for the treatment or cc diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, concreased TAT expression, particularly cancers such as breast cancer, cc colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder cc cancer, maclanoma and leukaemia. TAT nucleic acids may further be cused as hybridisation probes, in chromosome and gene mapping, in cc chromosome identification and in gene therapy. The present sequence cc crepresents a TAT nucleic acid of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or
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(first

cDNA sequence #410 encoding novel human secreted protein.

Human secreted protein; hyperproliferative disorder; autoimmune disorder; immune deficiency disorder; blood disorder; inflammatory disorder; infectious disorder; gene therapy; antimicrobial; hepatotropic; immunosuppressive; antirheumatic; ss. immunosuppressive;

29-MAR-2001; 2001WO-US010485

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06-APR-2000; 2000US-0195604P

GENETICS INST INC

Wong GG, Clark HF, Gulukota K, Graham Fechtel JR; ۳ Agostino 3 Howes SH, Resnick

WPI; 2002-010900/01

New polynucleotides encoding secreted asthma, HIV and Crohn's disease. proteins useful for treating e.g.

Page 291; 391pp; English.

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The present invention relates to the isolation of novel cDNA sequences

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                                                                                                                                                                                 The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (ABI99202 to ABI99912, encoding the protein sequences in ABB57020 to ABS7374) or by determining the expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition-improving drugs or therapeutics for ischaemic diseases. ABI9913 and ABI99914 represent primers for a mouse ischaemic condition related sequence, which are used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
                                                                                                                                                Sequence
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                   SEQ ID
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Seki N, 1
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24-JAN-2002; 2002US-0350435P.
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2003-395539/38.
DB; ADA55145.
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                                      f, Sugiyama T,
J, Isono Y,
Yoshikawa T,
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Hio Y, Otsuka K, Nagai K, Ir
Otsuka M, Nagahari K, Masuho
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disease; gene; ss.
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New polynucleotides encoding full-length polypeptides, e.g. secretory and/or membrane proteins, useful for developing medicines for diseases in which the gene is involved, or as target molecules for gene therapy.

Claim 1; SEQ ID NO 1074; 205pp; English.

The present invention relates to novel human secretory or membrane proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-ADA54071). The coding sequences are useful in the gene therapy of diseases caused by abnormalities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease.

Sequence 1988 BP; 519 A; 504 C; 584 G; 381 T; 0 U; 0 Other;

Query Match 81.6%; Score 1652.4; DB 10; Length 1988; Best Local Similarity 91.5%; Pred. No. 0; Matches 1831; Conservative 0; Mismatches 1; Indels 168; Gaps 1;

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                                                  New 1995 cDNA, useful Alzheimer's diseases,
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The present invention describes an isolated PRO nucleic acid (I). Also described: (I) a vector comprising (I); (2) a host cell comprising the vector of (I); (3) a process for producing a PRO polypeptides; (4) an isolated PRO polypeptide; (5) a chimeric molecule comprising the polypeptide of (4) fused to a heterologous amino acid sequence; (6) an antibody which specifically binds to a polypeptide of (4); (7) a composition of matter comprising a polypeptide of (4), an agonist or antagonist of the polypeptide or an antibody that binds to the polypeptide in combination with a carrier; (8) an article of manufacture comprising a container, a label on the container and a composition of matter of (7); (9) a method of treating an immune related disease in a mammal; (10) a method for determining the presence of a PRO polypeptide in a sample suspected of having the polypeptide; (11) a method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New PRO polynuclectides and polypeptides, useful in useful in diagnosing and treating an immune related disease, e.g. systemic lupus erythematosus, rheumatoid arthritis, diabetes mellitus or asthma and in stimulating an immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human; PRO; immune related disease; inflammatory immune response; immune response stimulation; antiallergic; antianaemic; antiarthritic; antiasthmatic; antidiabetic; antiinflammatory; antipsoriatic; antitheumatic; antithyroid; CNS; dermatological; gastrointestinal; haemostatic; hepatotropic; immunostimulant; immunosuppressive; muscular; nephrotropic; neuroprotective; osteopathic; respiratory; vasotropic; nephrotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
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                                                cc diagnosing an immune related disease or an inflammatory immune response cl in mammal; (12) a method of identifying a compound that inhibits or minics the activity of or expression of a gene encoding a PRO polypeptide c minics the activity of or expression of a gene encoding a PRO polypeptide c and (13) a method of stimulating the immune response in a mammal. The CPRO sequences have antiallergic, antiansemic, antiarchritic, antirheumatic, antidabetic, antiinflammatory, antipsoriatic, antirheumatic, antichyroid, CNS, dermatological, gastrointestinal, c antirheumatic, hepatotropic, immunostimulant, immunosuppressive, muscular, c nephrotropic, neuroprotective, osteopathic, respiratory, vasotropic and c virucide activities, and can be used in gene therapy. The nucleic acid c virucide activities, and can be used in gene therapy. The nucleic acid c useful in diagnosing and treating an immune related disease and in c stimulating an immune response. The present sequence represents a human c PRO nucleotide sequence from the present invention.
   Sequence 1807
BP; 476 A; 497 C; 523
G; 311
T; 0 U;
   0 Other;
                                                                                                                                                                                                                                                                                                                                                                                          polypeptide
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740 721 661 620 601 560 541 500 481 440 421 380 361 320 301 260 241 200 181 140 121 80 61 20 CAAAGCAGCTATGGGCAGCAGCCTCCCACTAGTTACCCCACCCCAAACTGGATCCTACAGC TCTCAGCAGAACACCTATGGGCAACCGAGCAGCTATGGACAGCAGAGTAGCTATGGTCAA TCCTACCCTCCTACCAGCTATTCCTCTACACAGCCGACTAGTTATGATCAGAGCAGTTAC TCCTACCCTCCTACCAGCTATTCCTCTACACAGCCGACTAGTTATGATCAGAGCAGTTAC AACTACAGTTATCCCCAGGTACCTGGGAGCTACCCCCATGCAGCCAGTCACTGCACCTCCA AGTCAACCTCAATCTAGCACAGGGGGGTTACAACCAGCCCAGCCTAGGATATGGACAGAGT CAGCAGCCAGCAGCCACTGCACCTACAAGACCGCAGGATGGAAACAAGCCCACTGAGACT CAGGCCTCCTATGCAGCTCAGTCTGCATATGGCACTCAGCCTTGCTTATCCAGCCTATGGG CCTGTCCAGGGGTATGGCACTGGTGCTTATGATACCACCACTGCTACAGTCACCACCACCACC TCTTATGGACAGCCTCCCACTGGTTATACTACTCCAACTGCCCCCCAGGCATACAGCCAG GATGTCAGCTATACCCAGGCTCAGACCACTGCAACCTATGGGCAGACCGCCTATGCAACT TATGCACAGACCACCCAGGCATATGGGCAACAAAGCTATGGAACCTATGGACAGCCCACT TATGCACAGACCACCCAGGCATATGGGCAACAAAGCTATGGAACCTATGGACAGCCCACT GACGGACGTTGAGAGAACGAGGAGGAAGGAGAAAATGGCGTCCACGGATTACAGTACC GACGGACGTTGAGAGAACGAGGAGGAAGGAGAAAATGGCGTCCACGGATTACAGTACC CAAAGCAGCTATGGGCAGCAGCCTCCCACTAGTTACCCCACCCCAAACTGGATCCTACAGC CAGGCCTCCTATGCAGCTCAGTCTGCATATGGCACTCAGCCTGCTTATCCAGCCTATGGG CCTGTCCAGGGGTATGGCACTGGTGCTTATGATACCACCACTGCTACAGTCACCACCACC TCTTATGGACAGCCTCCCACTGGTTATACTACTCCAACTGCCCCCAGGCATACAGCCAG GATGTCAGCTATACCCAGGCTCAGACCACTGCAACCTATGGGCAGACCGCCTATGCAACT TATAGCCAAGCTGCAGCGCAGCAGGGCTACAGTGCTTACACCGCCCAGCCCACTCAAGGA 120 CAGCAGCCAGCCACTGCACCTACAAGACCGCAGGATGGAAACAAGCCCACTGAGACT 780 739 720 679 540 79 799 660 619 600 559 499 480 439 420 379 360 319 300 259 240 199

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Query Match Best Local Simi Matches 1787;

Similarity

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13; Length 1807 Indels

219;

Gaps

Conservative

0; Mismatches Score 1557.4; Pred. No. 0;

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1920	GGCTTTGGTGGAGGAAGACGAGGTGGCCCTGGGGGGCCCCCTGGACCTTTGATGGAACAG	1861
1860	AGSTGSCCSTGSTGSAGACAGAGSTGSCTTCCGTGSTGSCCGGGGCATGGACCGAG 	o a
6	GTGGCATGCGGGAGGAAGAGGTGGCCTCATGGATCGTGGTGGTCCCGGTGG	54
80	GGTGGCATGCGGGGAGGAGAGAGGTGGCCTCATGGATCGTGGTGGTCCCCGGTGGAATGTTC	74
1740 1540	GAAGGCTTCCTCCCGCCACCCTTTCCGCCCCCGGGTGGTGATCGTGGCAGAGGTGGCCCT	1681 1481
44	GTGGAAACCAGAACTTCGCCTGGAGAACAGAGTGCAACCAGTGTA	42
1680	:Agaacttcgcctggagaacagagtgcaaccagtgtaaggccc	6
1620 1420	CCCTCTGGAGGAAGGACTCCAGCACCGAGCTGGAGACTGGCAGTGTCCCAATCCGGGT	ω G
1560 1360	GCCCGTGGAGGAGATAGAGGAGGCTTCCCTCCAAGAGGACCCCGGGGTTCCCGAGGGAAC	1501
1300	CACTCCGTGGAGGTCCAGGAGGCCCAGGAGGTCCTGGGGGA	1241
1500	CCACTCCGTGGAGGTCCAGGAGGCCCAGGAGGTCCTGGGGGACCCATGGGTCGCATGGGA	1441
1440 1240	CCTCCAATGAACAGTATGCCGGGTGGTCTGCCACCCCGTGAGGGCAGAGGCATGCCACCA	1381
1380	CCTTGCTCGGAAGA CCTTGCTCGGAAGA	1321
1320 1120	CAAGGCTC CAAGGCTC	9 9
1260	ATGAACAAGAGAACTGGGCAACCCATGATCCACATCTACCTGGACAAGGAAACAGGAAAG	0 0
1200	AATGACAGTGTGACTCTAGATGATCTGGCAGACTTCTTTAAGCAGTGTGGGGTTGTTAAG	1141 941
1140 940	GGCCCACCTGTAGATCCAGATGAAGACTCTGACAACACTGCAATTTATGTACAAGGATTA 11- 	മെ
880	GACCCATGGATGAAGGACCAGATCTTGATCTA	œ
1080	GAGCGAGGTGGCTTCAATAAGCCTGGTGGACCCATGGATGAAGGACCAGATCTTGATCTA	1021
848		
1020	CGTGGAGGCATGAGCAGAGGTGGGCGGGGGAGGACGCGCGGTGGAATGGGCAGCGCTGGA	
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960	GGAGAAACCGGAGCATGAGTGGCCCTGATAACCGGGGCAGGGGAAGAGGGGGATTTGAT	901
848		4
900	CAGGACCACCCCAGTAGCATGGGTGTTTATGGGCAGGAGTCTGGAGGATTTTCCCGGACCA	
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840	GCTCCAAGTCAATATAGCCAACAGAGCAGCAGCTACGGGCAGCAGAGTTCATTCCGA	781

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1. /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2. /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3. /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4. /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5. /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6. /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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Sequence 18, Appl
Sequence 1657, Ap
Sequence 6382, A
Sequence 13361, A
Sequence 1062, A
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ALIGNMENTS

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APPLICATION NUMBER: FR 92/06123 FILING DATE: 20-MAY-1992 ATTORNEY/AGENT INFORMATION: NAME: Weiser, Gerard J. REGISTRATION NUMBER: 19,763 REFERENCE/DOCKET NUMBER: 989.6121P TELECOMMUNICATION INFORMATION: TELEPHONE: 215-875-8383 TELEPHONE: 215-875-8394 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:	COUNTRY: USA ZIP: 19102 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: AEDIT 1.0 DOS text editor CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/343,443B FILING DATE: 18-NOV-1994 CLASSIFICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: FILING DATE: 19-MAY-1993	Trommation: Trommatics, A Trom	; Sequence 1, Application US/08343443B ; Patent No. 5968734
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2012; Conservative 0; Mismatches
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TYPE: nucleic acid
STRANDEDRESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 25..1992
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                                                                               GGTGGAGACAGAGGTGGCTTCCGTGGTGGCCGGGGCATGGACCGAGGTGGCTTTGGTGGA 1872
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                        AGAGGACGACGTGGAGGACCTGGAAAAATGGATAAAGGCGAGCACCGTCAGGAGCGCAGA 1992
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Sequence 13696, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSITITE OF INVENTION: WITH HUMAN DISEASE, METHODS OF FILE REFERENCE: CLOOL307

CURRENT PILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOSTWARE: FASHSEEQ for Windows Version 4.0

SEQ ID NO 13696
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; ORGANISM: Human
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Sequence 5044, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF TITLE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: 00/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTMARE: FastSEQ for Windows Version 4.0

SEQ ID NO 5044

LENGTH: 1785

TYPE: DNA

ORGANISM: Human

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PAPPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
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CURRENT APPLICATION NUMBER: US/09/949,01
CCURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER: OF SEQ ID NOS: 207012
SOFTWARE: PASISEQ for Windows Version 4.
SEQ ID NO 1954
LENGTH: 1783
TYPE: DNA
ORGANISM: Human
US-09-949-016-1954
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Best Local Similarity
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TTTGGTGGAGGAAGACGAGGTGGCCCTGGGGGGGCCCCTGGACCTTTGATGGAACAGATG
                                                                                                                                                                                        GGCATGCGGGGAGGAAGAGGTGGCCTCATGGATCGTGGTGGTCCCGGTGGAATGTTCAGA
                                                                                                                                                                                                                                                                               GGCTTCCTCCCGCCACCCTTTCCGCCCCCCGGGTGGTGATCGTGGCAGAGGTGGCCCTGGT
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                                                                                                             GGTGGCCGTGGTGGAGACAGAGGTGGCTTCCGTGGTGGCCGGGGGCATGGACCGAGGTGGC
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                                                                                                                                                                                                                                                        GGCTTCCTCCCCACCCTTCCCACCCCCGGGTGATCATGGCAGAGGTGGCCCTGGT
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                                                                                                                                                               GGCATGTGGGGAGGAAGAGGTGGCCTCATGGATCATGGTGGTCCCGGTGGAATGTTCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTTGATGGGAAAGATTTTCAAGGGAGCAAACTTAAAGTCTCCCTTGCTCGGAAGAAGCCT 1383
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US-08-437-027-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 4641
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEPAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 2412 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 18, Application Patent No. 5670317
                                                                                                                                                                                                                                                                                              Matches 819;
                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: cDNA to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1185 ...
STREET: New York
STATE: New York
STATE: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Landanyi, Marc
APPLICANT: Gerald, William
TITLE OF INVENTION: A DIAGNOSTIC TEST FOR TEST FOR THE DESMOPLASTIC
TITLE OF INVENTION: SMALL ROUND CELL TUMOR
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 2412 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1641 TTTGGTGGAGGAAGACAAGGTGGCCCTGGGGGGCCCCC-GGACCTTTGATGTAACCAATG 1699
 181
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                                                                                                                                                                                   73 GCAGCGCAGCAGGGCTACAGTGCTTACACCGCCCAGCCCACTCAAGGATATGCACAGACC
                                                                                                                                                                                                                                           13 GAGAACGAGGAGGAAGAGAAAATGGCGTCCACGGATTACAGTACCTATAGCCAAGCT
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ACCCAGGCTCAGACCACTGCAACCTATGGGCAGACCGGCCTATGCAACTTCTTATGGACAG
                                ACCCAGGCTCAGACCACTGCAACCTATGGGCAGACCGCCTATGCAACTTCTTATGGACAG
                                                                                                   ACCCAGGCATATGGGCAACAAAGCTATGGAACCTATGGACAGCCCACTGATGTCAGCTAT
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                                                                                                                                                                                                                                                                                              Conservative
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100.0%; Pred. No. 1.4e-210;
tive 0; Mismatches 0;
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FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                  US-09-513-999C-1657
Sequence 1657, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
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                                                                                                ; FEATURE:
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; LOCATION: 56..454
US-09-513-999C-1657
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APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
                                           Matches
                                                         Query Match
Best Local
                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                      TYPE: DNA
                                                                                                                                                                                   LENGTH: 454
                                          435;
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                                           Conservative
                                                         20.9%;
                                           0,
                                           Score 424; DB 4; Pred. No. 2.4e-104; 0; Mismatches 0;
                                                                    Length 454;
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                       Sequence 66382, Ap
Patent No. 6812339
                                                                                                                                                                                                                                                                             319
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
                                                                                                                                                      Query Match
Best Local S
Matches 367
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SEQ ID NO 66382
LENCTH: 601
TYPE: DNA
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                          AGCCAAGCTGCAGCGCAGCAGGGCTACAGTGCTTACACCGCCCAGCCCACTCAAGGATAT 123
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                                                                                                                                                        Conservative
                                                                                                                                                                         18.0%;
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Pred. No. 4.3e-88;
1; Mismatches 6
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GTCAGCTATACCCAGGCTCAGACCACTGCAACCTATGGGCAGACCGCCTATGCAACTTCT

243 195

GCACAGACCACCCAGGCATATGGGCAACAAGCTATGGAACCTATGGACAGCCCACTGAT 183

GCACAGACCACCCAGGCATATGGGCAACAAAGCTATGGAACCTATGGACAGCCCATTGAT

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9 US-09-880-107-3769
10 US-09-880-1706-1081
10 US-09-873-319-717
9 US-09-872-830A-49
9 US-09-872-830A-49
17 US-10-094-749-1074
3 18 US-10-485-115-182496
9 14 US-10-198-846-9847
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Sequence 1, Appli
Sequence 3769, Ap
Sequence 1081, App
Sequence 717, App
Sequence 49, Appl
Sequence 410, Appl
Sequence 1074, Ap
Sequence 182496,
Sequence 9847, Ap
Sequence 8001, Ap
Sequence 8001, Ap
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5.0	5.7	5.7	5.7	6.3	.4	6.4		7.1		8.7				8.9		8.9		9.2	9.3	9.3	10.7	12.5	12.6	12.8	12.8	13.2	13.3	15.3	18.3	19.0	19.7	20.3	23.7
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2734	e 145,	145,	Sequence 145, App	297, 1	Sequence 1576, Ap	24470,	Sequence 2865, Ap	19297,	Sequence 19709, A		Sequence 58, Appl	Sequence 649, App	Sequence 114301,			111659		17973,	•	Sequence 2572, Ap	Sequence 488, App	Sequence 25438, A	18163,	e 4463		481,		669, 7	10259	Sequence 24705, A	œ	•	Sequence 9557, Ap

ALIGNMENTS

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, NAME/KEY: CDS
; LOCATION: (44)..(2011)
; OTHER INFORMATION: EWS
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APPLICANT: JENAPHARM GmbH & Co. KG
TITLE OF INVENTION: Methods for Determining
FILE REFERENCE: Pat 3684/11
CURRENT APPLICATION NUMBER: US/10/791,017A
CURRENT FILING DATE: 2004-03-02
NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 2390
                                                                                                                                                    Query Match 100.0%; Score 2025; Best Local Similarity 100.0%; Pred. No. 0; Matches 2025; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/10791017A Publication No. US20040197827A1
                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Homo sapiens
8
                    61 TATAGCCAAGCTGCAGCGCAGCAGGGCTACAGTGCTTACACCGCCCCAGCCCCAGCCCAAGGA 120
TATAGCCAAGCTGCAGCGCAGCAGGGCTACAGTGCTTACACCGCCCAGCCCACTCAAGGA
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RESULT 2
US-09-800-107-3769
; Sequence 3769, Application
; Patent No. US20020142981A1
; GENERAL INFORMATION:
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
FITTLE OF INVENTION: Gene Expression Profiles in
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR PILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR APPLICATION NUMBER: US 60/237,054
                                                                                                                                                                                                                 APPLICANT: Horne, Darca ... APPLICANT: Vockley, Joseph "DOLICANT: Scherf, Uwe "Toric Inc
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; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3769
; LENGTH: 2390
; TYPE: DNA
; ORGANISM: Homo sapiens
; PEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 X66899
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APPLICANT: Kulkarni, Prakash
APPLICANT: Kulkarni, Prakash
APPLICANT: Kulkarni, Prakash
APPLICANT: Getzenberg, Robert H.
APPLICANT: Maga, Iwao
APPLICANT: Maga, Iwao
APPLICANT: Yamamoto, Jun
TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic
TITLE OF INVENTION: Hyperplasia Using Gene Expression Profiles
FILE REFERENCE: 44921-5029-US
CURRENT APPLICATION NUMBER: US/09/873,319A
CURRENT FILING DATE: 2001-06-05
EARLIER APPLICATION NUMBER: US 60/223,323
EARLIER FILING DATE: 2000-08-07
NUMBER OP SEQ ID NOS: 755
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 717
LEUGTH: 2390
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
PEATURE: PROPRESSION Genbank Accession No. US20030134324A1 X66899
US-09-873-319-717
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US-09-873-319-717
; Sequence 717, Application US/09873319A
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; GENERAL INFORMATION:
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100.0%; Pred. No. 0;
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APPLICANT: Genetics Institute, Inc.
APPLICANT: Wong, Gordon G.
APPLICANT: Clark, Hilary
APPLICANT: Clark, Hilary
APPLICANT: Pechtel, Kim
APPLICANT: Agostino, Michael J.
APPLICANT: Howes, Steven H.
APPLICANT: Howes, Steven H.
APPLICANT: Graham, James R.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
FILE REFERENCE: GIN 6402
CURRENT APPLICATION NUMBER: US/09/822,830A
CURRENT APPLICATION NUMBER: US/09/822,830A
CURRENT FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 600/195,604
PRIOR APPLICATION NUMBER: 600/195,604
PRIOR APPLICATION NUMBER: 601/195,604
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 631
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 49
LENGTH: 2176
TYPE: DNA
ORGANISM: Homo sapiens
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US-09-822-830A-49/c
US-09-822-830A-49/c
; Sequence 49, Application US/09822830A
; Patent No. US20020142952A1
; GENERAL INFORMATION:
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GENERAL INFORMATION:

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IITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOV

FILE REFERENCE: GIN 6402

CURRENT APPLICATION NUMBER: US/09/822,830A

CURRENT FILING DATE: 2000-04-06

NUMBER OF SEQ ID NOS: 631

SOFTWARE: Patentin Ver. 2.0

LENGTH: 2273

TYPE: DNA

ORGANISM: Homo sapiens
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1074
LENGTH: 1988
TYPE: DNA
CORGANISM: Homo sapiens
US-10-094-749-1074
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US-10-094-749-1074
                                                                                                                                                                                                                                                                                           APPLICANT: OTSUKA, KAORU
APPLICANT: NAGAI, KEJICHI
APPLICANT: IRIE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHIKO
APPLICANT: OTSUKA, MOTOVUKI
APPLICANT: VOSHIKAWA, TSUTOMU
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NUMBER: US/10/094,749
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
PRIOR FILING DATE: 2001-09-14
NUMBER: DESCRIPTION SEQ ID NOS: 3381
                                                                                                                  Query Match
Best Local Similarity
Matches 1831; Conserv
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APPLICANT:
APPLICANT:
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APPLICANT: SUGIYA
APPLICANT: OTSUKI
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ISHII, SHIZUKO
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OTSUKI, TETSUJI
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91.5%;
                                                                                                                  Score 1652.4;
Pred. No. 0;
0; Mismatches
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                                                                                                                                                        DB 17;
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                                                                                                                      Indels 168;
                                                                                                                                                        Length 1988;
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TGATCCACATCTACCTGGACAAGGAAACAGGAAAGCCCAAAGGCGATGCCACAGTGTCCT
                                                                                                                          GTGGACCCATGGATGAAGGACCAGATCTTGATCTAGGCCCACCTGTAGATCCAGATGAAG
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                                                TGGCAGACTTCTTTAAGCAGTGTGGGGGTTGTTAAGATGAACAAGAGAAACTGGGCAACCCA
                                                                                                                GTGGACCCATGGATGAAGGACCAGATCTTGATCTAGGCCCACCTGTAGATCCAGATGAAG
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      GENERAL INFORMATION:

APPLICANT: LA ROSA, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Chou, Yihua

APPLICANT: Chou, Yihua

APPLICANT: Chou, Yihua

APPLICANT: Chou, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecul

TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(5322)B

CURRENT APPLICATION NUMBER: US/10/425,11:

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 182496

LENGTH: 763

TYPE: DNA
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ORGANISM: Zea mays
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and

Other Molecules

Associated With

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GAGGACCTGGAAAAATGGATAAAGGCGAGCACCGTCAGGAGGGCCAGAGAGTCGGCCCTACT
                                                                                                                                                                                        GCCCTGGGGGGCCCCCTGGACCTTTGATGGAACAGATGGGAGGAAGAAGAAGAAGAGGACGTG
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RESULT 9
US-10-198-846-9847
US-10-198-846-9847, Application US/10198846
; Sequence 9847, Application US/10198846
; Publication No. US20030099974A1
; GENERAL INFORMATION:
; APPLICANT: Lilite, James
; APPLICANT: Wang, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, ANI
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
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Best Local Similarity
Matches 661; Conserv
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NAME/KEY: unsure

LOCATION: (1)...(763)

OTHER INFORMATION: unsure at all n
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Pred. No. 9.3e-174;
0; Mismatches 51;
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                AND METHODS PREVENTION,
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; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,84
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FASESEQ for Windows Version 4.
; SEQ ID NO 9847
; SEQ ID NO 9847
; LENGTH: 2299
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-198-846-9847
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               CGAGCTGGAGACTGGCAGTGTCCCAATCCG
                                                                           CCTCCAAGAGGACCCCGGGGTTCCCGAGGGAACCCCTCTGGAGGAGGAAACGTCCAGCAC
                                                                                                                    GGAGGTCCTGGGGACCCATGGGTCGCATGGGAGGCCGTGGAGGAGATAGAGGAGGCTTC
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 CGAGCTGGAGACTGGCAGTGTCCCAATCCG
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Pred. No. 9.9e-156;
0; Mismatches 0;
                             1617
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; Sequence 8001, Application US/09864761
; Patent No. US20020048753A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Penn, Sharron G.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL;
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Acomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
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FOR

RESULT 10 US-09-864-761-8001

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TYPE: DNA

GRGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: MAP TO ACO18774.3

OTHER INFORMATION: EXPRESSED IN BAIN, SIGNAL = 2.1

OTHER INFORMATION: EXPRESSED IN BEAIN, SIGNAL = 3.4

OTHER INFORMATION: EXPRESSED IN FITAL LIVER, SIGNAL = 3.4

OTHER INFORMATION: EXPRESSED IN FITAL LIVER, SIGNAL = 3.4

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.1

OTHER INFORMATION: EXPRESSED IN LING, SIGNAL = 2.4

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.9

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.9

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.9

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.9
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Best Local S
Matches 521
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SOFTWARE: Annomax Sequence List
SEQ ID NO 8001
LENGTH: 540
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR APPLICATION NUMBER: US 09/774,203
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OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/USO1/00665
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/USO1/00668
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/USO1/00663
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/USO1/00662
OR APPLICATION NUMBER: PCT/USO1/00662
OR APPLICATION NUMBER: PCT/USO1/00662
OR FILING DATE: 2001-01-30
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APPLICATION NUMBER: GB 24263.6
FILING DATE: 2000-10-04
APPLICATION NUMBER: US 60/236,359
FILING DATE: 2000-09-27
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                                                                                                                                                               GCACAGACCACCCAGGCATATGGGCAACAAAGCTATGGAACCTATGGACAGCCCACTGAT
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GTCAGCTATACCCAGGCTCAGACCACTGCAATCTATGGGCAGACCGCCTATGCAACTTCT
                                                                                                                      GCACAGACCACCAGGCATATGGGCAACAAAGCTATGGAACCTATGGACAGCCCATTGAT
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Pred. No. 1e-139;
0; Mismatches 11;
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APPLICANT: Hyseq, Inc.
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUE
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRA
FILE REFERENCE: 2041-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOPTWARE: FASESEQ for Windows Version 3.0
SEQ ID NO 27690
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US-09-918-995-27690
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Best Local
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TYPE: DNA
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                                                                                  GGAGGAGGAACGTCCAGCACCGAGCTGGAGACTGGCAGTGTCCCAATCCGGGTTGTGGA
                                                                                                                            GGAGGAGATAGAGGAGGCTTCCCCTCCAAGAGGACCCCCGGGGTTCCCCGAGGGAACCCCCTCT
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FOR

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FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 9557
LENGTH: 568
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Best Local S
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Publication No. US20030073623A1
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NAME/KEY: misc feature
LOCATION: (1).T. (568)
OTHER INFORMATION: n = A,T,C
-09-918-995-9557
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TITLE OF INVENTION: NOVEL NUCLEIC
TITLE OF INVENTION: FROM VARIOUS
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ORGANISM: Homo sapiens
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AACTTAAAGTCTCCCTTGCTCGGAAGAAGCCTCCAATGAACAGTATGCGGGGTGGTCTGC 1411
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                                                                                                                                                         ACATCTACCTGGACAAGGAAACAGGAAAGCCCCAAAGGCGATGCCACAGTGTCCTATGAAG 129:
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ilarity 95.5%;
Conservative
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Pred. No. 1.1e-129;
0; Mismatches 20;
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CDNA LIBRARIES
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PRIOR APPLICATION NUMBER: PCT/USO1/00665
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR FILING DATE: 2001-01-30
PRIOR PPLICATION NUMBER: PCT/USO1/00662
PRIOR PILING DATE: 2001-01-30
PRIOR PPLICATION NUMBER: PCT/USO1/00661
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR PILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
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PRIOR FILING DATE: 2001-01-30
PRIOR PPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PPLICATION NUMBER: PCT/US01/00664
PRIOR PPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PILING DATE: 2001-01-30
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 7766
LENGTH: 505
TYPE: DNA
ORGANISM: HOMO S
FEATURE:
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APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OP INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES
TITLE OP INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
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OTHER INFORMATION: MAP TO AL162311.1
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.5
OTHER INFORMATION: EXPRESSED IN LINNG, SIGNAL = 2.5
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.4
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.7
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.7
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.7
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Sequence 3668, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBT
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3868
LENGTH: 401
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US-09-918-995-3868
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Best Local Similarity
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ORGANISM: Homo
-09-918-995-3868
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                                               GAAGGAGAGAAAATGGCGTCCACGGATTACAGTACCTATAGCCAAGCTGCAGCGAGCAG
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                            GAAGGAGAAAATGGCGTCCACGGATTACAGTACCTATAGCCAAGCTGCAGCGCAGCAG
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Pred. No. 4.1e-106;
0; Mismatches 1;
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Pred. No. 1.2e-109;
0; Mismatches 19;
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               GCATATGGCACTCAGCCTGCTTATCCAGCCTATGGGCAGCA
                                                   GCTTATGATACCACCACTGCTACAGTCACCACCCAAGCCTCCTATGCAGCTCAGTCT
                                                                    GCTTATGATACCACCACCACCAGTCACCACCACCAGGCCTCCTATGCAGCTCAGTCT
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RESULT 15 US-09-864-761-24705

Sequence 24705, Application US/09864761 Patent No. US20020048763A1

GENERAL

APPLICANT:

APPLICANT: Penn, Sharron G. INFORMATION:

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CURRENT PILLING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR PILING DATE: 2000-02-04
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-30
PRIOR PILING DATE: 2000-09-37
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR PRIOR PRIOR DATE: 2001-01-30
PRIOR PRIOR DATE: 2001-01-30
PRIOR PRIOR PRIOR DATE: 2001-01-30
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Hanzel, David K.
Chen, Wensheng
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OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.1

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.8

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.4

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.4

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.1

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.4

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.9

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OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.6

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NUMBER OF SEQ ID NOS: 49117

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ALIGNMENTS

REFERENCE AUTHORS REFERENCE AUTHORS ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 1 CR604952 LOCUS S ORIGIN FEATURES COMMENT DEFINITION Query Match Best Local Sin Matches 2025; TITLE JOURNAL TITLE JOURNAL REMARK source 1 GACGGACGTTGAGAGAACGAGGAGGAAGGAAAAATGGCGTCCACGGATTACAGTACC - Web: www.genoscope.cns.fr) 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a Genoscope. Direct Submission Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2157) Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished CR604952 CR604952 CR604952 CR604952 division of Invitrogen Homo sapiens CR604952.1 GI:50485759 HTC; CNSLT_CDNA. Faraday Avenue 2 (bases 1 to 2157) Contact : Similarity Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Conservative /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CSODIO10Y112" /tissue_type="Placenta_Cot_25 /plasmid="pCMVSPORT_6" Location/Qualifiers 100.0%; Score 2025; 100.0%; Pred. No. 0; tive 0; Mismatches mRNA linear HTC 21-JUL-2004 2 of Placenta Cot 25-normalized DΒ 25-normalized" 0, ω •• Length Indels 2157; <u>.</u> Gaps 60 0

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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
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BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
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2 (bases 1 to 2314)
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Db	ORIGIN	FEATURES BOU	AUTHORS TITLE JOURNAL COMMENT	JOURNAL REMARK	OKGANISM REFERENCE AUTHORS TITLE	ACCESSION VERSION KEYWORDS SOURCE	RESULT 3 CR625247 LOCUS DEFINITION	D Q	g Qy	Qy db	gg Qy	ß &	D
Hest Local Similarity 99.9%; Pred. No. 0; Best Local Similarity 99.9%; Pred. No. 0; Matches 2022; Conservative 0; Mismatches 0; Indels 3; Gaps 1; Matches 2022; Conservative 0; Mismatches 0; Indels 3; Gaps 1;	/moi_type="mxxxx" /db xref="taxon:9606" /clone="CSODEOO5YF11" /tissue type="placenta" /plasmid="pCMVSPORT_6"	into the l was norma division			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; (CE 1 (bases 1 to 2159) RS Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization	•	N	1981 CAGGAGCGCAGAGATCGGCCCTACTAGATGCAGAGACCCCGGCAGA 2025	1921 ATGGGAGGAAGAAGAAGAAGAAGGACGTGGAGGACCTGGAAAAATGGATAAAGGCGAGCACCGT 1980 	1861 GGCTTTGGTGGAGGAAGACGAGGTGGCCCCTGGGGGCCCCCTGGACCTTTGATGGAACAG 1920	1801 AGAGGTGGCCGTGGTGGAGACAGAGGTGGCTTCCGTGGTGGCCGGGGGCATGGACCGAGGT 1860	1741 GGTGGCATGCGGGGAAGAAGATGGCCTCATGGATCGTGGTGGTCCCGGTGGAATGTTC 1800	1685 GAAGGCTTCCTCCCGCCACCCTTTCCGCCCCCGGGTGGTGATCGTGGCAGAGGTGGCCCT 1744
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Homo sapiens (human)
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Mammalla; Eutheria; Primates; Catarrhini; Hor
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a
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1 (bases 1 to 2070)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CR602561 2070 bp mRNA linear full-length cDNA clone CS0DI068YN23 of Placenta Cot of Homo sapiens (human).
CR602561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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HTC; CNSLT_cDNA.
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                                   GGACAGCCCACTGATGTCAGCTATACCCCAGGCTCAGACCACTGCAACCTATGGGCAGACC
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GCCTATGCAACTTCTTATGGACAGCCTCCCACTGGTTATACTACTCCAACTGCCCCCCAG
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/db_xref="taxon:9606"
/clone="CSODI068YN23"
/tissue_type="placenta_Cot_2
/plasmid="pCMVSPORT_6"
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                                CCAGCCTATGGGCAGCAGCCAGCAGCCACCTGCACCTACAAGACCGCAGGATGGAAACAAG
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/db_xref="taxon:9606"
/clone="CSODI064YE15"
/tissue_type="placenta_Cot_2
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                                         ATGGACCGAGGTGGCTTTGGTGGAGGAGGAGGAGGTGGCCCTGGGGGGGCCCCCTGGACCT
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229 GCCTATGCAACTTCTTATGGACAGCCTCCCACTGGTTATACTACTCCAACTGCCCCCCAG 288	109 CCCACTCAAGGATATGCACAGACCACCCAGGCATATGGGCAACAAAGCTATGGAACCTAT 168	/ Match 96.8%; Score 1961; DB 3; Length 2126; Local Similarity 99.8%; Fred. No. 0; 1e8 1974; Conservative 0; Mismatches 0; Indels 3; Gaps 1; 19 GATTACAGTACCTATAGCCAAGCTGCAGCGCAGGGGCTACAGTGCTTACACCGCCCAG 108 1		NotI-olig was digest the pCM	Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue 2 (bases 1 to 2126) Genoscope. Direct Submission Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage:	_	CR610888 full-length (human). CR610888 CR610888.	1969 GGCGAGCACCGTCAGGAGCGCAGAGATCGGCCCTACTAGATGCAGAGACCCCGCAGA 2025
Q B Q B Q B	S B S B S	5 8 8 8	8 8 8 8	B & B &	B & B &	5	9 9 9 9 9 9 9 9 9 9	g Q
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		FEATURES source		COMMENT	JOURNAL	REFERENCE AUTHORS TITLE	REMARK	AUTHORS TITLE JOURNAL	REFERENCE	SOURCE ORGANISM	VERSION KEYWORDS	DEFINITION	CR593724	SECULT A	B &			QV dd	8 8		8	Db	Ş	B &	B 8	αb
/cione="CSUDIO11YOU5" /tissue_type="Placenta Cot 25-normalized"	/organism="Homo варiens" /mol_type="mRNA" /db_xref="taxon;9606"	.	into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.	end enriched, double-strand cDNA was digested with Not I and cloned	Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY Cedex - FRANCE (E-mail : seqref@genoscope.cns.fr		Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue		Mammalia; Eutheria; Primates; 1 (bases 1 to 2073)	Homo sapiens (human) Homo sapiens Chicagonia	CR537/24.1 GI:50474531 HTC; CNSLT_CDNA.	full-length cDNA clone CSODIO117005 of Placenta Cot 25-rof Homo, sapiens (human).	linear		196 Y GGCGAGCACCGTCAGGAGCGCAGAGATCGGCCCTACTAGATGCAGAACCCCGCAGAA 2043	TI ISA TIGGAACAGA TIGGAAGGAAGAAGAAGAAGAAGAAGA TIGGAAGAACATAAAA TIGGAATAAAAAAAAAAAAAAAAAAAAAAAAAA	TTGATGGAACAGATGGGAGGAAGAAGAAGAGGAGGACGTGGAAGAAAATGGATAAA	1849 ATGGACCGAGGTGGCTTTGGTGGAGGAAGACGAGGTGGCCCTGGGGGGGCCCCCTGGACCT 1908	1738 GGTGGAATGTTCAGAGGTGGCCGTGGTGGAGACAGAGGTGGCTTCCGTGGTGGCCGGGGC 1797	AGAGGTGGCCCTGGTGGCATGCGGGGAAGAGAGATGGCCTCATGGATCGTTGGTGGTCCCC	1729 AGAGGTGGCCTGGTGGCATGCGGGAAGAAGAGGTGGCCTCATGGATCGTGGTGGTCGCC 1788	1618 GCCCAAAGCCTGAAGGCTTCCTCCCGCCACCCTTTCCGCCCCGGGTGGTGATCGTGGC 1677	1669 GCCCCAAAGCCTGAAGGCTTCCTCCCGCCACCCTTTCCGCCCCCGGGTGGTGATCGTGGC 1728	1609 CCCAATCCGGGTTGTGGAAACCAGAACTTCGCCTGGAGAACAGAGTGCAACCAGTGTAAG 1668	1549 TCCCGAGGGAACCCCTCTGGAGGAGAGACGTCCAGCACCGAGCTGGAGACTGGCAGTGT 1608	
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1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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1 (bases 1 to 2083)

Li.W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization
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Direct Submission
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1 (bases 1 to 2236)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation
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          GATGAAGACTCTGACAACAGTGCAATTTATGTACAAGGATTAAATGACAGTGTGACTCTA
                                                 AAGCCTGGTGGACCCATGGATGAAGGACCAGATCTTGATCTAGGCCCACCTGTAGATCCA
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AKEN full-length enriched library, clone:9430031M11

product:Ewing sarcoma homolog, full insert sequence.

AK034755

AK034755.1 GI:26084174

AK034755.1 GI:26084174

Mus musculus (house mouse)

Mus musculus (house mouse)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA
Meth. Enzymol. 303, 19-44 (1999)
99279253
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                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                     Chordata;
Rodentia;
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                                                                     Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute c Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yoko Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Group Phase I & II Team.
Analysis of the mouse transcriptome of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2373)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsunoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Kokazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                             cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Functional annotation of a Nature 409, 685-690 (2001)
                                                                                                                                                                                                                                                                                     prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="12 days embryo"
43. _2011
                                                                                                                                                                                                  organism="Mus musculus"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                     tissue_type="embryonic body between diaphragm region"
                                                                                                                 /clone="9430031M11"
                                                                                                                                      /db_xref="FANTOM_DB:9430031M11"
/db_xref="taxon:10090"
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/note="Ewing sarcoma homolog (MGD|MGI:99960, GB|NM_007968, evidence: BLASTN, 99%, match=2172)
putative"
polyA_signal 2368.2363
/note="putative"
polyA_site 2373
/note="putative"

polyA_site 2373
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87.4%; Score 1769.8; DB 3; Length 2373;
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Similarity GACGGACGTTGAGAGAACGAGGAGGAAGGAGAAAATGGCGTCCACGGATTACAGTACC GCAGCAGCCAGCCAGCCACCTGCACAAGACCGCAGGATGGAAACAAGCCCCACTGAGAC CCAAGCTCCAAGTCAATATAGCCAACAGAGCAGCAGCTACGGGCAGCAGAGTTCATTCCG CTCTCAGCAGAACACCTATGGGCAACCGAGCAGCTATGGACAGCAGAGTAGCTATGGTCA ATCTTATCCTCCTACCAGCTACTCCTCTTCACAGCCGACTAGTTACGATCAGAGCAGTTA ATCCTACCCTCCTACCAGCTATTCCTCTACACAGCCGACTAGTTATGATCAGAGCAGTTA TAACTACAGTTATCCCCAGGTACCTGGGAGCTACCCCATGCAGCCAGTCACTGCACCTCC TAGTCAACCTCAATCTAGCACAGGGGGTTATAACCAACCCAGCCTAGGATATGGACAGAG TAGTCAACCTCAATCTAGCACAGGGGGTTACAACCAGCCCAGCCTAGGATATGGACAGAG CCAGCAGCCAACAGCCACCGCACCTACCAGACCACAGAGGATGGTAACAAGCCTGCTGAGAC GCAGGCC CCAGGCCTCTATGCAGCTCAGTCTGCATATGGCACTCAGCCTGCTTATCCAGCCTATGG GCCTGTCCAGGGGTATGGCACTGGTGCTTATGATACCACCACTGCTACAGTCACCACCAC TTCTTATGGACAGCCTCCCACTGGTTATACTACTCCAACTGCCCCCCAGGCATACAGCCA TGATGTCAGCTATACTCAGGCTCAGACCACTGCCACCTACGGGCAGACTGCATATGCAAC TGATGTCAGCTATACCCAGGCTCAGACCACTGCAACCTATGGGCAGACCGCCTATGCAAC TATGCACAGACCACCCAGGNCATATGGGCAACAAAGCTATGGAACCTATGGACAGCCTAC TATGCACAGACCACCCAGG-CATATGGGCAACAAAGCTATGGAACCTATGGACGCCAC TATAGTCAAGCTGCAGCCCAGCAGGGCTACAGTGCTTACACCGCCCAGCCAACTCAAGGA TATAGCCAAGCTGCAGCGCAGCAGGCTACAGTGCTTACACCGCCCAGCCCACTCAAGGA GACGGACGTTGAGAGAACGAGGAAGGCGAGAAAATGGCGTCCACGGATTACAGTACC ACAGGACCACCCCAGTAGCATGGGTGTTTATGGGCAGGAGTCTGGAGGATTTTCCCGGACC **ACAAAGCAGCTATGGGCAGCAGCCTCCTACTAGTTACCCCCCCTCAGACTGGATCCTACAG** 87.4%; nilarity 93.2%; Conservative CTTACGCAGCTCAGACTGCATATGGCACCCAGCCTGCCTACCCCACCTATGG Score 1769.8; Pred. No. 0; 0; Mismatches **;** 4. 306 299 126 120 6 839 779 659 909 599 546 539 486 426 419 366 359 246 239 186 846 726 999 899

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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

[AL Nature 420, 563-573 (2002)

[CE 6 (bases 1 to 2107)

[AR Nature 470, Full-length cDNAs

[AL Nature 420, 563-573 (2002)

[CE 6 (bases 1 to 2107)

[CE 6 (bases 1 to 2107)

[CE 7]

[CATRINCI, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayateu, N., Hiramoto, K., Furuno, M., Hanagaki, T., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Suzuki, H., Tagami, M., Tagawa, A., Shiraki, T., Sogabe, Y., Sibbata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Tejima, Y., Toya, T., Yamamura, T., Yashinishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Pxnloration Research Group, RIKEN Genomic Sciences Center (GSC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequencing p
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High-efficiency full-length cDNA cloning
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Please visit our web site (http://genome.gsc.riken.jp/) fo details.
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Similarity 93.3%;
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TCAGACCACTGCAACCTATGGGCAGACCGCCTATGCAACCTTCTTATGGACAGCCTCCCAC
                                       ATATGGGCAACAAAGCTATGGAACCTATGGACAGCCTACTGATGTCAGCTATACTCAGGC
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="18 days pregnant adult"
17. ~1984
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/db_xref="taxon:10090"
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Pred. No. 0;
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Mus musculus 12 days embryo spinal enriched library, clone:C530046A18
                                                                                                                                                                                                                                                                                                                 HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
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AK049743.1 GI:26093614
HTC; CAP trapper.
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to
                                                                                                                                                         Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Mammalia; Eutheria;
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

AL Nature 420, 563-573 (2002)

CE 6 (bases 1 to 2269)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagqaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hayashida, K., Hayatsu, N., Hiramoto, S., Kogawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Toh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saito, R., Saito, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Tomaru, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Takahashi, F., Takaku-Akahira, S., Muramateu, M., and Hayashizaki, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rigeromic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama 230-0045, Japan (E-mail:genome-resegsc.riken.jp, URLihttp://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                      URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
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Please visit our web site for further details.
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  /note="Ewing sarcoma homolog (MGD|MGI:99960,
evidence: BLASTN, 99%, match=2172)
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2251. .2256
                                                                                                    /organism="Mus musculus"
/mol_type="mRNA"
                                                                                                                                                                                                              clone="C530046A18"
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clone CSODIO39YJ24 5-PRII
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BX325713.2 GI:46280663
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
2 mail: segrefogenoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the PCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSOASO12ZHO2QP1&c=10589.f.
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1 (bases 1 to 1049)
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GGCCTCCTATGCAGCTCAGTCTGCATATGGCACTCAGCCTGCTTATCCAGCCTATGGGCA
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                                                                          TGTCCAGGGGTATGGCACTGGTGCTTATGATACCACCACTGCTACAGTCACCACCACCCA
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Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
0DI039YJ24 5-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="CS0DI039YJ24"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone_Tib= strand cDNA was primed with a NotI-oligo(dT)
/note="Tist strand cDNA was primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                               48.7%;
                                                                                                                                                                                                                                                                                                                                                                                                8;
                                                                                                                                                                                                                                                                                                                                                                                                Score 987; DB 5;
Pred. No. le-238;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                            DB 5;
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AUTHORS
TITLE
JOURNAL
COMMENT
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ORGANISM
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VERSION
KEYWORDS
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For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSODC004BC11QP1&c=10589.f.
Location/Qualifiers
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GATGTCAGCTATACCCAGGCTCAGACCACTGCAACCTATGGGCAGACCGCCTATGCAACT
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                                                                    TCCTACCCTACCAGCTATTCCTCTACACAGCCGACTAGTTATGATCAGAGCAGTCAC
                                                                                                                                                                     AACTACAGTTATCCCCAGGTACCTGGGAGCTACCCCATGCAGCCAGTCACTGCACCTCCA
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llarity 98.1%;
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/clone="CSDDC004YE22"
/clone="CSDDC004YE22"
/tissue type="NeuroblasToMA COT 25-NORMALIZED"
/clone Tib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a Notl-clipe(dT)
/note="five prime end enriched, double-strand cDNA was
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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|mol_type="mRNA"
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Pred. No. 3.8e-236; 
6; Mismatches 12;
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960 CGTGGASGCATGACMYRAGGTGGGCSGGGAGGACGCGGTGGAATGG 1008	961 CGTGGAGGCATGAGCAGAGGTGGGCGGGGAGGACGCGGTGGAATGG 1009	900 GGAGAGAACCGGAGCATGAGTYGGCCTGATAACCGGGGSAGGGGGAAGAGGGGGATTTGAT 959	901 GGAGAGAACCGGAGCATGAGTGGCCCTGATAACCGGGGCAGGGGAAGAGAGGGGGATTTGAT 960	840 CAGGACCACCCCAGTAGCATGGGTGTTTATGGGCAGGAGTCTGGAGGATTTTCCGGACCA 899	841 CAGGACCACCCCAGTAGCATGGGTGTTTATGGGCAGGAGTCTGGAGGATTTTTCCGGACCA 900	780 CAAGCTCCAAGTCAATATAGCCAACAGAGCAGCAGCAGCAGCAGCAGCAGAGTTCATTCCGA 839	781 CAAGCTCCAAGTCAATATAGCCAACAGAGCAGCAGCAGCTACGGGCAGCAGAGTTCATTCCGA 840

Search completed: February 20, 2005, 16:17:50 Job time : 5987.34 secs

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Result
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Perfect score:
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                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1010.4
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11541.209 Million cell updates/sec
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Copyright (c) 1993 - 2005 Compugen Ltd.
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AR080100
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BC072442
AK056309
CCR456490
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AK026270
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                 BT007796 Synthetic
AX714390 Sequence
AX05681 Homo sapi
BC004817 Homo sapi
BC004817 Homo sapi
CQ867364 Sequence
A36460 Sequence
A36460 Sequence
A3441125 Sequence
CX68899 H.sapiens
CQ850483 Sequence
AX117624 Homo sapi
CQ730352 Sequence
BC072442 Homo sapi
CQ730352 Sequence
BC072449 Homo sapi
CX456499 Homo sapi
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BC011048 Homo sapi
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50.2	50.5	50.8	51.8	54.6	55.3	55.3	55.6	55.6	58.9	64.6	74.1	74.1	74.1	77.0	77.0	80.8	80.8	85.0	86.9	86.9	86.9	88.5	89.7	89.7	89.7
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AC105889	AC079549	AC149218_2	AC099212	AC079494	AC079538	AC079538	AC079537	AC150903	AJ719366	CQ434162	AC106522	AC098231	AC128482	AC121282	AC113313	AC110672	AC109802	CQ721057	BC083960	MMEWS	AX305537	BC068226	AC011221	AL596087	AC018774
AC105889 Rattus no	AC079549 Mus muscu	Continuation (3 of	AC099212 Rattus no	AC079494 Mus muscu	AC079538 Mus muscu	AC079538 Mus muscu	AC079537 Mus muscu	AC150903 Mus muscu	AJ719366 Gallus ga	CQ434162 Sequence	AC106522 Rattus no	AC098231 Rattus no	AC128482 Rattus no		AC113313 Mus muscu	AC110672 Canis fam		CQ721057 Sequence	BC083960 Xenopus 1	X79233 M.musculus	AX305537 Sequence	BC068226 Mus muscu	AC011221 Homo sapi	Humar	AC018774 Homo sapi

ALIGNMENTS

FEATURES BOURCE	COMMENT	TITLE JOURNAL	JOURNAL REFERENCE AUTHORS	TITLE	REFERENCE	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 BT007796 LOCUS DEFINITION
expression clones generated by BD Blosciences Clontech and the Harvard Institute of Proteomics. Each CDS has been cloned in two forms: with and without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD In-Pusion(TM) cloning system between the Sall and HindIII sites of the pDNR-DUAL vector. Additional sequences in the clone: 'ACC' after Sall site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before HindIII site to maintain reading frame. Clone distribution: http://bioinfo.clontech.com/orfclones. 11971 /organism="synthetic construct" /mol_type="mRNA" /db_xref="taxon:32630" /clone="GH00297L1.0" /clone="GH00297L1.0" Clone="TDD Creator(TM) CDS Library derived from MGC	Circle, Palo Alto, CA 94303, USA This CDS clone is a part of a collection of human full length	Koundinya,M., kapnael,J., Moreira,D., Kelley,T., Labaer,J., Lin,Y., Phelan,M. and Farmer,A. Direct Submission Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Meadow	Vipublished Unpublished 2 (bases 1 to 1971) Kalnine, N., Chen, X., Rolfs, A., Halleck, A., Hines, L., Eisenstein, S., Kalnine, N., Chen, X., Rolfs, A., Halleck, A., Hines, L., Eisenstein, S.,	<pre>RoundInya,M., kapnael,J., Moreira,D., Kelley,T., Labaer,J., Lin,Y., Phelan,M. and Farmer,A. Cloning of human full-length CDSs in BD Creator(TM) System Donor Vector</pre>	other sequences; artificial sequences. 1 (bases 1 to 1971) Kalnine, N., Chen, X., Rolfs, A., Halleck, A., Hines, L., Eisenstein, S.,	BT007796 BT007796.1 GI:30584430 BT007796.1 construct synthetic construct	BT007796 1971 bp mRNA linear SYN 13-MAY-2003 Synthetic construct Homo sapiens Ewing sarcoma breakpoint region 1

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 GTGCAACCAGTGTAAGGCCCCAAAGCCTGAAGGCTTCCTCCCGCCACCCTTTCCGCCCCC 720
                                              TGGAGACTGGCAGTGTCCCAATCCGGGTTGTGGAAACCAGAACCTTCGCCTGGAGAACAGA
                                                                                         AAGAGGACCCCGGGGTTCCCGAGGGAACCCCTCTGGAGGAGGAAACGTCCAGCACCGAGC
                                                                                                         AAGAGGACCCCGGGGTTCCCCGAGGGAACCCCTCTGGAGGAGGAAACGTCCAGCACCGAGC 600
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/note="Vector: pDNR-Dual"
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/db_xref="G1:30584431"
/translation="MASTDYSTYSQAAAQQGYSAYTAQPTQGYAQTTQAYGQQSYGTY
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Patent: EP 1293569-A 1074 19-MAR-2003;
Helix Research Institute (JP) ; Resear
Biotechnology (JP)
Location/Qualifiers
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Sequence 1074 from Patent EP1293569.
AX714390
AX714390.1 GI:29889342
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CATCTACCTGGACAAGGAAACAGGAAAGCCCAAAGGCGATGCCACAGTGTCCTATGAAGA 300
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/mol_type="unassigned DNJ
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                                                                                                                                                                                                                                                                                                            AK056681
AK056681.1 GI:16552152
oligo capping; fis (full insert
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                      1988 bp mRNA linear Homo sapiens cDNA FLJ32119 fis, clone PEBLM1000034, to RNA-BINDING PROTEIN EWS.
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Mammalia; Eutheria;
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Primates;
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                                                                                                                                                                                                                                                                                                                                                   sequence)
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highly similar
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18 Isogal, T., Otsuki, T. and Sugiyama, T.
Direct Submission
Submitted (24-OCT-2001) Takao Isogal, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: RAB and
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문 밁 밁 8 Ś ई 밁 ঠ 밁 S 밁 S 문 ঠ S 밁 र् Ś 밁 밁 S 밁 Ś 밁 맑 ई 밁 8 밁 8 밁 ORIGIN Matches 1012; Query Match Best Local Similarity 1400 1340 1220 1160 1100 1700 1640 1580 1520 1460 1280 1040 481 421 361 301 241 980 920 960 841 781 661 601 541 181 121 800 901 61 CATGGATGAAGGACCAGATCTTGATCTAGGCCCACCTGTAGATCCAGATGAAGACTCTGA CCCACCCACTGCCAAGGCTGCCGTGGAATGGTTTGATGGGAAAGATTTTTCAAGGGAGCAA 360 CATCTACCTGGACAAGGAAACAGGAAAGCCCAAAAGGCGATGCCACAGTGTCCTATGAAGA CATCTACCTGGACAAGGAAACAGGAAAGCCCAAAGGCGATGCCACAGTGTCCTATGAAGA CAACAGTGCAATTTATGTACAAGGATTAAATGACAGTGTGACTCTAGATGATCTGGCAGA CAACAGTGCAATTTATGTACAAGGATTAAATGACAGTGTGACTCTAGATGATCTGGCAGA AGGACGCGGTGGAATGGGCAGCGCTGGAGAGCGAGGTGGCTTCAATAAGCCTGGTGGACC AGGACGCGGTGGAATGGGCAGCGCTGGAGAGCGAGGTGGCTTCAATAAGCCTTGGTGGACC GGGGCCCCCTGGACCTTTGATGGAACAGATGGGAGGAAGAAGAAGAGGAGGACGTGGAGGACC 960 GGGTGGTGATCGTGGCAGAGGTGGCCCTGGTGGCGCATGCCGGGGAAGAAGAGGTGGCCTCAT 780 TGGAGACTGGCAGTGTCCCAATCCGGGTTGTGGAAACCAGAACTTCGCCTGGAGAACAGA AAGAGGACCCCGGGGTTCCCCGAGGGAACCCCTCTGGAGGAGGAAACGTCCAGCACCGAGC 1399 ACCCCGTGAGGGCAGAGGCATGCCACCACCACTCCGTGGAGGTCCAGGAGGCCCCAGGAGG ACTTANAGTCTCCCTTGCTCGGAAGAAGCCTCCAATGAACAGTATGCGGGGGTGGTCTGCC 420 CTTCTTTAAGCAGTGTGGGGTTGTTAAGATGAACAAGAGAACTGGGCAACCCATGATCCA CTTCTTTAAGCAGTGTGGGGTTGTTAAGATGAACAAGAGAACTGGGCAACCCCATGATCCA CATGGATGAAGGACCAGATCTTGATCTAGGCCCACCTGTAGATCCAGATGAAGACTCTGA CCGTGGTGGCCGGGGCATGGACCGAGGTGGCTTTGGTGGAGGAAGACGAGGTGGCCCTGG 900 GGATCGTGGTGGTCCCGGTGGAATGTTCAGAGGTGGCCGTGGTGGAGACAGAGGTGGCTT 840 GTGCAACCAGTGTAAGGCCCCAAAGCCTGAAGGCTTCCTCCCGCCACCCTTTCCGCCCCC TGGAGACTGGCAGTGTCCCAATCCGGGTTGTGGAAACCAGAACTTCGCCTGGAGAACAGA TCCTGGGGGACCCATGGGTCGCATGGGAGGCCGTGGAGGAGAATAGAGGAGGCTTCCCTCC 1339 TCCTGGGGGACCCATGGGTCGCATGGGAGGCCGTGGAGGAGAGATAGAGGAGGCTTCCCTCC 540 ACTTAAAGTCTCCCTTGCTCGGAAGAAGCCTCCAATGAACAGTATGCGGGGTGGTCTGCC Conservative PPMNSMRGGLPPREGRGMPPPLRGGPGGPGGPGGPMGRMGGRGGDRGGFPPRGPRGSR GNPSGGSNVOHRAGDMQCPNPGCGNQNEWTTECNQCKAPKPEGFLPPPPPPGPDRG RGGPPGGMRGGGLMDRGGPGGMPGRGGRGGNGGFRGGRGMDRGGFGGGRRGGPGGPP GPLMEQMGGRRGGPGMDKGEHRQERRDRPY" 100.0%; 0 Score 1012; DB 9; Pred. No. 6.9e-197; Mismatches Length 1988; Indels 0; Gaps 1459 1279 480 1159 1099 1039 919 660 1219 180 120 859 60 1759 1699 1639 1579 1519 240 979

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Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
                                                                                                                                                     Clone distribution: MGC clone distribution through the I.M.A.G.B. Consortium/LIML at: Series: IRAK Plate: 3 Row: 1 Column: 6 This clone was selected for full length sec passed the following selection criteria: He
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission

Submitted (21-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2182)
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BC004817
BC004817.1 GI:13435962
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2182 bp mRNA linear PRI 29-JUN-2004
Homo sapiens Ewing sarcoma breakpoint region 1, transcript variant
EWS, mRNA (cDNA clone MGC:5432 IMAGB:3449145), complete cds.
                                                                                                                                                                                                                                                                                                                                      Web site: http://www.hgsc.bcm.tmc.edu/cdna/Contact: amg@bcm.tmc.edu
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Huly
Kowis, C.R., Sneed, A.J., Martin, R.G., Muz
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing Center
Center code: BCM-HGSC
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
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/organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                Location/Qualifiers
                                                                                                                                                              length sequencing because riteria: Hexamer frequency
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                                                                                                                                                                                                                                               information can be found http://image.llnl.gov
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                TCCTGGGGGACCCATGGGTCGCATGGGAGGCCGTGGAGGAGATAGAGGAGGCTTCCCCTCC
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 ACCCCGTGAGGGCAGAGGCCATCCACCACCACTCCGTGGAGGTCCAGGAGGCCCCAGGAGG
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/db_xref="MIM:133450"
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/clone="MGC:5432 IMAGE:3449145"
/tlssue_type="Placenta, choriocarcinoma"
/clone_Tib="NIH_MGC_10"
/lab_host="DH10B"
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Mismatches 0;
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Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Sequence 1 from Patent EP1455190.
CQ867364 GI:51997589
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                                                                                                                                                                                                                                                                                                               Modulation of the activity of nuclear
Patent: EP 1455190-A 1 08-SEP-2004;
Schering Aktiengesellschaft (DE)
Location/Qualifiers
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                       /organism="Homo sapiens"
/mol_type="unassigned DN/
/db_xref="taxon:9606"
44...2014
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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RESULT 8 AX411125 LOCUS DEFINITION Sequence 3772 from Patent W00229103. ACCESSION ACCESSION AX411125 ACCESSION AX411125 GETWORDS SOURCE ORGANISM Homo sapiens (human) ORGANISM AUTHORS TITLE TITLE Gene expression profiles in liver cancer PATURES FEATURES SOURCE (SENE LOGIC INC (US) FEATURES SOURCE (Jorganisms "Homo sapiens" JOURNAL GENE LOGIC INC (US) FEATURES SOURCE (Jorganisms "Homo sapiens" JORGANISM AUTHORS ALVARES, C., Horne, D., Peres-da-Silva, S. and Vockley, J.G. JORGANISM FEATURES JOURNAL GENE LOGIC INC (US) JORGANISM JORGA	Qy 661 GTGCAACCAGTGTAAGGCCCAAAGCCTGAAGGCTTCCTCCCGCCACCCTTTCCGCCCCC 720	Qy 241 CATCTACCTGGACAAGGAAACAGGAAAGCCCAAAGGCGATGCCACAGTGTCCTATGAAGA 300 1221 CATCTACCTGGACAAGGAAACAGGAAAGCCCAAAGGCGATGCCACAGTGTCCTATGAAGA 1280 1221 CATCTACCTGGACAAGGAAACAGGAAAAGCCCAAAGGCGATGCCACAGTGTCCCTATGAAGA 1280 Qy 301 CCCACCCACTGCCAAGGCTGCCGTGGAATGGTTTGATGGAAAAGATTTTCAAGGGAGCAA 360 Qy 361 ACTTAAAGTCTCCCTTGCTCGGAAGAAGCCTCCAATGAACAGTTTTCAAGGGAGCAA 1340 Qy 361 ACTTAAAGTCTCCCTTGCTCGGAAGAAGCCTCCAATGAACAGTATGCGGGGTGGTCTGCC 420

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/note="EMBL/GenBank Accession No. X66899"
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SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL MEDLINE REFERENCE AUTHORS TITLE JOURNAL COMMENT FEATURES FEATURES SOURCE DO19A P019A	RESULT 9 HSEWS LOCUS DEFINITION ACCESSION VERSION
Homo sapiens (human Homo sapiens Eukaryota; Metazoa; Metazoa; Metazoa; Mammalia; Eutheria; 1 Delattre,O., Zucman Peter,M., Kovar,H., and Thomas,G. Gene fusion with an translocation in hu Nature 359 (6391), 9239623 2 (bases 1 to 2371 Delattre,O., Direct Submission Submitted (26-MAY-1 Inst. Curie, 26 rue On Sep 23, 194 thi Location/O. (cone="194" /clone="194" /clone="1	HSEWS H.sapiens X66899 X66899.1
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an) a; Chordata; Crania; Crania; Primates; Catar an, J., Plougastel, J., Joubert, I., de an ETS DNA-binding human tumours , 162-165 (1992) 71) 71) 71) 71) 71) 72) 73) 74 75 76 77) 71) 71) 71) 72) 73) 74 75 76 77 77 77 77 78 78 78 78 78	2390 bp
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Patent: EP 1447413-A 952 18-AUG-2004;
Research Association for Biotechnology
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                   Bource
                                                                                                                                                                                                                       Isogai, T. and Yamamoto, J.

Lisubmission

Lisubmission

Lisubmisted (15-7UL-2003) Takao Isogai, FLJ Project(HRI Team); 2-6-7

Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan

(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of

Economy, Trade and Industry of Japan; cDNA full insert sequencing:

Research Association for Biotechnology (RAB); cDNA library

construction: Helix Research Institute (HRI) (supported by Japan

Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,

HRI, and Biotechnology Center, National Institute of Technology and

Evaluation; clone selection for full insert sequencing: HRI and

RAB; annotation: Reverse Proteomics Research Institute, HRI and
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AK127524
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Mammalia, Eutheria, Primates,
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ogai, T. and Yamamoto, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human cDNA sequencing project
/cell_type="coronary artery smooth muscle cells (HCASMC)"
/clone_lib="HCASM2"
/note="cloning vector: pME18SFL3-primary culture, coronary
                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                        Location/Qualifiers
                                                                     clone="HCASM2008154"
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clone HCASM2008154,
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961 TGGAAAAATGGATAAAGGCGAGCACCGTCAGGAGCGCAGAGATCGGCCCTAC 1012
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artery smooth muscle cells"

ORIGIN		
Query M. Best Low Matches	atch 99.7%; Score 1008.8; DB 9; Length 2026; cal Similarity 99.8%; Pred. No. 3.1e-196; 1010; Conservative 0; Mismatches 2; Indels 0;	Gaps 0;
\$	GCGCTGGAGAGCGAGGTGGCTTCAATAAGCC	GACC 60
망	B AGGACGCGGTGGAATGGGCAGCGCTGGAGAGCGAGGTGGCTTCAATAAGCCTGG	GAC
i S	0	12
מט	98 CATGGATGAAGGACCAGATCTTGATCTAGGC	CIGA 95
Ş	N	CAGA 18
В	5	CAGA 1017
\$	181 CTTCTTTAAGCAGTGTCGGGGTTGTTAAGATGAACAAGAGAACTGGGCAACCCCATGATC	=CA 24
DЪ	;;:	ATCCA 1077
Ş	241 CATCTACCTGGACAAGGAAACAGGAAAGCCCAAAGGCGATGCCACAGTGTCCTAT	RATGAAGA 300
DЬ	ACCTGGACAAGGAAACAGGAAAAGCCCAAAAGGCGATGCCACAGTGTCC	AAGA 1137
Ş	301 CCCACCCACTGCCAAGGCTGCCGTGGAATGGTTTGATGGGAAAGATTTTCAAGGGAGCAA	AGCAA 360
ДЬ	38 CCCACCCACTG	GCAA 1197
Ş	361 ACTTAAAGTCTCCCCTTGCTCGGAAGAAGCCTCCAATGAACAGTATGCGGGGTGGTCTGC	TIGCC 420
Ъ	CTTAAAGTCTCCCTTG	TGCC 1257
γ	421 ACCCCGTGAGGGCAGAGGCATCACCACCACTCCGTGGAGGTCCAGGAGGCCCA	CAGGAGG 480
	CCCCGTGAGGGCAGAGGCATGCCACCACCACTCCGTGGAGGTCCAGGAGGCCC	GAGG 1317
Ş	481 TCCTGGGGGACCCATGGGTCGCATGGGAGGCCGTGGAGGAGGATAGAGGAGGCTTCCCTC	— ი
	18 TC	crcc 1377
8	41 AAGAGGACCCCGGGGTTCCCGAGGGAACCCCTCTGGAGGAGGAGGAAACGTCCAGGAC	CGAGC 600
	1378 AAGAGGACCCCGGGGGTTCCCCGAGGGAACCCCCTCTGGAGGAAAACGTCCAGCAC	GAGC 1437
Ş	601 TGGAGACTGGCAGTGTCCCAATCCGGGTTGTGGAAACCAGAACTTCGCCTGGAGAA	BAACAGA 660
DЬ	38 TGGAGACCTGCAGTGTCCCAATCCGGGTTGTGGAAACCAGAACTTCGCCTTGGAC	ξ: G-
Ş	TGCAACCAGTGTAAGGCCCCAAAGCCTGAAGGCTTCCTCCCGCCACCCTTTCCC	CCCCC 720
Db	98 GTGCAACCAGTGTAAGGCCCCAAAGGCTGAAGGCTTCCTCCCGCCACCCTTTCCC	6-
Qy .	721 GGGTGGTGATCGTGGCAGAGGTGGCCCTGGTGGCATGCGGGGAAGAAGAGGTGGCCTCAT	TCAT 780 .
Ъ	58	TCAT 1617
γQ	781 GGATCGTGGTCCCGGTGGAATGTTCAGAGGTGGCCGTGGTGGAGACAGAGGTGG	GCTT 840
DЬ	18 GGATCGTGGTGGTCCCGGTGGAATGTTCAGAGGTGGC	GCTT 1677
Ş	841 CCGTGGTGGCCGGGGCATGGATCGAGGTGGCTTTTGGTGGAGGAAGACGAGGTGGC	CCTGG 900
В	CGTGGTGGCCGGGGCATGGACCGAGGTGGCTTTGGTGGAGGAAGACGAGGTGGC	CCTGG 1737
Ş	901 GGGGCCCCTGGACCTTTGATGGAACAGATGGGAGGAAGAAGAGGAGGACGTGGAGGAC	3GACC 960
Ъ	1738 GGGCCCCCTGGACCTTTGATGGAACAGATGGGAGGAGAAGAAGAAGAGGACGTGGA	3GACC 1797
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Best Local Similarity 99.9
Matches 1012; Conservative
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Sequence 162
CQ730352
CQ730352.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent: WO 02068579-A 16286 06-SEP-2002, PE Corporation (NY) (115)
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Mammalia; Eutheria; Primates;
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Homo sapiens
Eukaryota; Metazoa;
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    TGGAGACTGGCAGTGTCCCAATCCGGGTTGTGGAAACCAGAACTTCGCCTGGAGAACAGA
                                                                         ACTTAAAGTCTCCCTTGCTCGGAAGAAGCCTCCAATGAACAGTATGCGGGGTGGTCTGCC
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                                                                                                                                                              TCCTGGGGGACCCATGGGTCGCATGGGAGGCCGTGGAGGAGATAGAGGAGGCTTCCCTCC
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16286 from Patent WO02068579.
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Pred. No. 1.2e-194;
0; Mismatches 0;
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buctow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsiah, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myars, R.M.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length
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                                                                           Direct Submission
Submitted (01-7UN-2004) National Institutes of Health, Mammalian Submitted (01-7UN-2004) Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
Email: cgapbs-r@mail.nih.gov
                      NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                               human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2164)
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Akhter.N., Ayele,K., Becketrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blatrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,B., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touthman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can be four through the I.M.A.G.E.G. Consortium/LINI at: http://image.llnl.gov Series: IRAK Plate: 174 Row: g Column: 18
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4885224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.nisc.nih.gov/
                                                                              CATGGATGAAGGACCAGATCTTGATCTAGGCCCACCTGTAGATCCAGATGAAGACTCTGA
                                                                                                                  CATGGATGAAGGACCAGATCTTGATCTAGGCCCACCTGTAGATCCAGATGAAGACTCTGA
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                                                                                                                                                                                                                                                                              Conservative
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/protein_id="AAH72442.1"
/db_xref="GI:48734727"
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/db_xref="LocusID:2130"
/db_xref="MIM:133450"
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/tissue type="Skin, melanotic me
/clone Iib="NIH MGC 72"
/lab_host="DH10B"
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/mol_type="mRNA"
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/db_xref="MIM:133450"
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Ota, T.,
                                                             oligo capping; fis (full insert sequence).
Homo sapiens (human)
Homo sapiens
                                                                                                                            AK056309 2189 bp
Homo sapiens cDNA FLJ31747 fis,
to RNA-BINDING PROTEIN EWS.
AK056309
                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                            AK056309.1 GI:16551673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTTCTTTAAGCAGTGTGGGGTTGTTAAGATGAACAAGAGAACTGGGCAACCCATGATCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGATCGTGGTGGTCCCGGTGGAATGTTCAGAGGTGGCCGTGGTGGAGACAGAGGTGGCTT
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    Suzuki, Y., Nishikawa, T.,
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                                                                                                                                                             mRNA linear clone NT2RI2007377,
    Otsuki,T.,
    Sugiyama, T., Irie, R.,
                                                                                                                                                             PRI 30-JAN-2004
highly similar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E 3 (bases 1 to 2189)

18 Ioogai, T., Otsuki, T. and Sugiyama, T.

19 Direct Submission

Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute,

Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

(B-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of

Economy, Trade and Industry of Japan; cDNA full insert sequencing:

Research Association for Biotechnology (RAB); cDNA library

construction: Helix Research Institute (HRI) (supported by Japan

Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,

HRI, and Biotechnology Center, National Institute of Technology and

Evaluation; clone selection for full insert sequencing: RAB and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ishibashi, T., Kanehori, K., Yosida, M., Watanabe, S., Ishida, S., Ono, Y., Hotuta, T., Hiraoka, S., Murakawa, K., Takiguchi, S., Kusano, J., Watanabe, M., Fujimori, K., Tanai, H., Ishida, M., Yamashita, H., Chiba, Y., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T.
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/clone_lib="NT2RI2"
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/note="cloning vector: pME18SFL3-mRNA from NT2 neuronal
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note="unnamed protein product"
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TITLE

FEATURES

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1713 GGGTGGTGATCGTGGCAGAGGTGGCCCTGGTGGCATGCGGGGAAGAAGAGGTGGCCTCAT 1772	13	٠
721 GGGTGGTGATCGTGGCAGAGGTGGCCCTGGTGGCATGCGGGGAGGAAGAGGTGGCCTCAT 780		_
6		
	1593	
601 TGGAGACTGGCAGTGTCCCAATCCGGGTTGTGGAAAACCAGAACTTCGCCTGGAGAACAGA 660	10	_
541 AAGAGGACCCCGGGGTTCCCGAGGGAACCCCTCTGGAGGAGGAAACGTCCAGCACCGAGC 600		
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481 TCCTGGGGGACCCATGGGTCGCATGGGAGGCCGTGGAGGAGATAGAGGAGGCTTCCCTCC 540		_
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421 ACCCCGTGAGGGCAGAGGCATGCCACCACCACTCCGTGGAGGTCCAGGAGGCCCCAGGAGG 480		_
3 ACTTAAAGTCTCCCTTGCTCGGAAGAAGCCTCCAATGAACAGTATGCGGGGTGGTCTGCC	1353	
361 ACTTAAAGTCTCCCTTGCTCGGAAGAAGCCTCCAATGAACAGTATGCGGGGTGGTCTGCC 420	_	_
1293 CCCACCCACGCCAAGGCTGCCGTGGAATGGTTTGATGGGAAAGATTTTCAAGGGAGCAA 1352		
301 CCCACCCACTGCCAAGGCTGCCGTGGAATGGTTTGATGGGAAAGATTTTCAAGGGAGCAA 360		_
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241 CATCTACCTGGACAAGGAAACAGGAAAGCCCAAAGGCGATGCCACAGTGTCCTATGAAGA 300		_
1173 CTTCTTTAAGCAGTGTGGGGTTGTTAAGATGAACAAGAGAACTGGGCAACCCATGATCCA 1232 ·		
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61 CATGGATGAAGGACCAGATCTTGATCTAGGCCCCACCTGTAGATCCAGATGAAGACTCTGA 120		
993 AGGAGGACGCGGTGGAATGGGCGCTGGAGAGCGAGGTGGCTTCAATAAGCCTGGTGGACC 1052	93	
1 AGGACGCGGTGGAATGGGCAGCGCTGGAGAGCGAGGTGGCTTCAATAAGCCTGGTGGACC 60		
fatch 98.4%; Score 996; DB 9; Length 2189; scal Similarity 98.8%; Pred. No. 1.3e-193; 1000; Conservative 0; Mismatches 12; Indels 0; Gaps 0;	Query Match Best Local Simi Matches 1000;	
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sanger Institute name: pGEM.EWSR1
Homo sapiens CDNA sequence. This sequence was generated as part of
The Wellcome Trust Sanger Institute program to isolate cDNA clones
representing the full length open reading frame of well annotated
protein coding genes on human chromosome 22. For more information
see http://www.sanger.ac.uk/HGP/Chr22/.
Location/Qualifiers
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Collins,J.E., Wright,C.L., Edwards,C.A., Davis,M.P.,
Cole,C.G., Goward,M.E., Aguado,B., Mallya,M., Mokrab.
Huckle,E.J., Beare,D.M. and Dunham,I.
Direct Submission
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CR456490.1 GI:47678510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (24-MAY-2004) Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: c22g@sanger.ac.uk Manuscript
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens EWSR1 full length open
(CDNA clone C22ORF:pGEM.EWSR1).
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(ORF) cDNA clone
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Query Match
Best Local Similarity
Matches 1000; Conser

98.4%; ilarity 98.8%; Conservative

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Score 996; DB 9; Length 2189; Pred. No. 1.3e-193; 0; Mismatches 12; Indels

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Aas70647 DNA encod
Abk84628 Human cDN
Abk64822 Human ben
Abh97274 Gene #377
Acn40903 Tumour-as
Adr07446 Full leng
Adp56333 Human PRO
Acn37537 Tumour-as
Aas62623 cDNA sequ
Abi99383 Mouse isc
Aal26725 Human bre
Acn8667 Breast ca
Aag50646 Human Ews
Ach40478 Human Ews
Ach40478 Human adu
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Aas62262 cDNA sequ
Adq86032 Human tum
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ALIGNMENTS

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RESULT 1 ADA53506

ADA53506;

20-NOV-2003

(first entry)

ADA53506 standard; cDNA; 1988

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Human coding sequence, SEQ ID 1074.

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Isogai T, Sugiyama T,
Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
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                                                                                     WPI; 2003-395539/38.
P-PSDB; ADA55145.
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24-JAN-2002; 2002US-0350435P.
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(REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                                                             Otsuki T, Wakamatsu A, Sato H, Hio Y, Otsuka K, Nagai K, Irie Otsuka M, Nagahari K, Masuho Y;
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                                                                                                                         Ishii S;
R, Tamechika
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New polynucleotides encoding full-length polypeptides, e.g. secretory and/or membrane proteins, useful for developing medicines for diseases which the gene is involved, or as target molecules for gene therapy.

'n

The present invention relates to novel human secretory or membrane proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-

Claim 1; SEQ ID

NO 1074; 205pp; English.

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1145 61

CATGGATGAAGGACCAGATCTTGATCTAGGCCCACCTGTAGATCCAGATGAAGACTCTGA CATGGATGAAGGACCAGATCTTGATCTAGGCCCCACCTGTAGATCCAGATGAAGACTCTGA

1086 120 1146 60 0

AGGACGCGGTGGAATGGGCAGCGCTGGAGAGCGAGGTGGCTTCAATAAGCCTGGTGGACC

Matches 1012; Query Match Best Local :

Similarity

100.0%; Score 1012; DB 6; 100.0%; Pred. No. 3e-233;

Conservative

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2176 BP; 413

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Other;

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Gaps

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RESULT 2
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ID AAS62262;
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                                                                         The present invention relates to the isolation of novel cDNA sequences completed encode human secreted proteins. The cDNA sequences have been completed from a variety of human tissues. The invention also provides a comethod for producing proteins from these polynuclectide sequences. The proteins are useful for identifying compounds that modulate their compounds that modulate expression of the polynuclectide sequences compounds that modulate expression of the polynucleotide sequences of creating diseases such as hyperproliferative disorders (e.g. cancer), commune deficiency disorders (e.g. severe combined immunodeficiency compounds that modulate expression of the invention are useful continued the secreted proteins. The sequences of the invention are useful continued disorders (e.g. severe combined immunodeficiency) commune disorders (e.g. multiple sclerosis), blood disorders (e.g. thrombocytopaenia), inflammatory disorders (e.g. arthritis) and confectious disorders (e.g. hepatitis). The polynucleotide sequences of the invention are also useful in gene therapy. AAS62388

Crepresent the cDNA sequences of the invention that encode for novel human continued to the continued for the invention that encode for novel human continued to the continued for the invention that encode for novel human continued to the continued for the invention that encode for novel human continued to the continued for the invention that encode for novel human continued for the invention that encode for novel human continued for the invention that encode for novel human continued for the invention that encode for novel human continued for the invention that encode for novel human continued for the invention that encode for novel human continued for the invention that encode for novel human continued for the invention that encode for novel human continued for the invention that encode for novel human continued for the invention that encode for novel human continued for the invention of the continued for the invention of the continued for the 
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1 K, Graham
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human; tumour-associated antigenic target; TAT; cytostatic;
                                   Human tumour-associated antigenic target (TAT) cDNA sequence #2904
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Matches 1012;

Similarity

100 100.0%;

Score 1012; Pred. No. 3. Mismatches

3.1e-233; DB 13;

0;

Gaps

1059 60 0,

Conservative

AGGACGCGGTGGAATGGGCAGCGCTGGAGAGCGAGGTGGCTTCAATAAGCCTGGTGGACC

Sequence 2372 BP;

628 A; 589 C; 668 G; 487 T; 0 U; 0 Other;

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CC target (TAT) muclaic acid comprising: (a) any of 4622 nucleatide
CC sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of
CC (a); (c) the complement of (a) or (b); (d) a sequence that has 80%
CC expence identity to (a)-(c); or (e) a sequence that hybridises to (a)-
CC (c). Also described: (l) an expression vector comprising the above
cc nucleatic acid; (2) a host cell comprising the above expression vector; (3)
CC a process for producing a polypeptide; (4) an isolated polypeptide
CC comprising: (a) an amino acid sequence encoded by any of the above
cc mucleatide sequences; (b) an amino acid sequence encoded by the full-
cC length coding region of the above nucleotide sequences; or (c) a sequence
CC having at least 80% identical to (a) or (b); (5) a chimeric polypeptide
CC comprising the above polypeptide fuels to a heterologous polypeptide; (6)
CC an isolated antibody; (a) a nisolated oligopeptide; (7) a process
CC for producing the antibody; (b) an isolated oligopeptide; (7) a process
CC the above polypeptide; (9) a tumour-associated antigenic target (7AT)
CC binding organic molecule that binds to the above polypeptide; (10) a
CC composition of matter comprising organic molecule; (10) a
CC composition of matter contained within the container; (12) methods of
CC the growth of the cell is at least in part dependent upon a growth
CC potentiating effect of the above protein; (13) a method of
CC potentiating effect of the above protein; (13) a method of
CC potentiating effect of the above protein; (13) a method of
CC potentiating effect of the above protein; (13) a method of
CC potentiating the protein in a sample suspected of containing the protein
CC described above; (15) methods of diagnosing the presence of a tumour in a
CC described above; (15) methods of binding an antibody, oligopeptide or
CC protein; and (17) a method of binding an antibody, oligopeptide or
CC protein; and (17) a method of binding an antibody, oligopeptide or
CC protein; are composition of methods of the above
CC prot
New nucleic acid molecule and encoded polypeptide, for diagnosing, preventing or treating cell proliferative disorders such as cancer
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Determining the hormonal effects of substances, used to identify pharmaceuticals, e.g. for treatment of androgen receptor dysfunction, from modulating interaction between nuclear receptors and Ewing sarcoma
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25-APR-2003; 2003US-0465692P
                                                                                                                                                                                                                                                                                                                                                                          Homo
                                                                                                                                                                                                                                                                                                                                                                                       numan; ss; gene; Ewing sarcoma; EWS; prostatic hypogonadism; androgen-resistance sundromo.
                                                                                                                                                  Claim 7; SEQ ID NO 1; 30pp; German.
                                                                                                                                                                                                                WPI; 2004-627861/61.
                                                                                                                                                                                                                               Obendorf M,
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                                                                                                                                                                                                                                                                                                                                                                                                               cDNA encoding the Ewing sarcoma protein SeqID
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/product=
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                                                                                                                                                                                                                                                                                                                                                                                          alopecia; acr
feminisation.
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This invention relates to a novel modulators that alter the interaction CC between the Ewing sarcoma protein (EWS) and its nuclear receptor, as well CC as the screening method thereof. Specifically, it refers to determining CC and identifying a hormonal effect brought about by test compounds that CC modulate either the binding of EWS to the nuclear receptor or the ligand-CC induced activity of this receptor. The present invention describes the nuclear receptors as including oestrogen, progesterone, thyroid hormone, CC vitamin D, and retinoic acid receptors, most preferably they are androgen CC receptors. Accordingly, these modulators may be used in the development CC diseases associated with receptor dysfunction such as prostatic cancer, alopecia, acne, hypogonadism and androgen-resistance syndrome e.g. CC test.cular feminisation. This method provides reliable, sensitive, CC simple, inexpensive and ragid assessment of the hormonal effects of these CC test compounds. This polynucleotide sequence is the cDNA encoding the human Ewing sarcoma protein of the invention.

Sequence 2390 BP; 646 A; 589 C; 668 G; 487 T; 0 U; 0 Other;

Length

2390

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CTTCTTTAAGCAGTGTGGGGTTGTTAAGATGAACAAGAGAACTGGGCAACCCATGATCCA
                                                   CAACAGTGCAATTTATGTACAAGGATTAAATGACAGTGTGACTCTAGATGATCTGGCAGA
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18-NOV-2004

(first entry)

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AQ506
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DT 25-M
DT 26-M
DT 26-M
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Chrc
KW mall
KW pris
                                       chromosomal translocation; chimeric; malignant melanoma; hum-fli-1; primittive peripheral neuroectodermal human chromosome 22; ss.
                 Homo sapiens
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26-MAY-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid of EWS gene and its hybrid(s) - contg. gene sequence involved in chromosomal trans-location, also derived mRNA, probes, fusion proteins etc., for diagnosis and treatment of Ewing sarcoma and melanoma.
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Thomas
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P-PSDB; AAR44555.
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rary (Stratagene cat.# 936206). The clone BF1AC5 was identified and
uenced. It represents the entire coding region and 3'-UTR of the Ews
e. (Updated on 25-MAR-2003 to correct PN field.)
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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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23-AUG-2000; 2000US-00649167.
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The invention relates to isolated polynucleotide (I) and polypeptide (II) gequences. (I) is useful as hybridisation probes, polymerase chain (C) and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed complete in the sequence tags for identifying expressed complete in the sequence tags for identifying expressed complete in the sequence tags for identifying expressed complete. (II) is useful in gene therapy techniques to restore normal complete in the sequence against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food complete in tissue, as molecular weight markers and as a food complete in the binding partners are useful in medical imaging of sites expressing (II). (II) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The complete and polymucleotide sequences have applications in complete and polymucleotide sequences have applications in the product of the invention of mutations and complete complete content types of data and products dependent on DNA and complete in the product of the sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the print of the print of the printer of the pri Claim 1; SEQ ID NO 6451; 103pp; English. biodiversity

Sequence 2388 BP; 628 A; 599 C; 668 G; 493 T; 0 U; 0 Other;

ftp.wipo.int/pub/published_pct_sequences

Matches 1011;

Conservative

o,

Query Match Best Local Similarity

99.8%;

Score 1010.4; Pred. No. 7.5e 0; Mismatches

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                                                                                              Detecting granulocyte activation by detecting genes associated with granulocyte activation, markers that is useful for monitoring disease
The invention relates to detecting (M1) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (Gs) identification chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated GC, where
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human cDNA
                                                                                                                                                                             Beazer-Barclay Y,
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CC differential expression of Gs is indicative of GCA. Also included are CC modulating (M2) GA by contacting GC with an agent that alters the CC expression of at least one gene in Gs; (2) screening (M3) for an agent CC tissue, an allergic response in a subject, exposure of a subject to a CC pathogen or sterile inflammatory disease using the gene expression CC pathogen or sterile inflammatory disease using the gene expression CC pathogen or sterile inflammatory disease, by detecting the level of CC expression of the gene is indicative of inflammation; (4) treating CC (M5) an inflammation (especially chronic) in a CC inflammatory disease, by contacting a tissue of gene (B) from Gs, where the level of expression in a subject, exposure of a subject to a gent that modulates the expression of gene (B) from Gs in the tissue. M1 CC is useful for detecting GCA; M2 is useful for modulating of a subject to a pathogen or sterile inflammation in a tissue, M4 is useful for detecting GA; M3 is useful for detecting an agent capable of modulating GCA preferably in an CC (especially chronic) in a tissue, an allergic response in a subject to a pathogen or sterile inflammation with an CC (especially chronic) in a tissue, an allergic response in a subject to a pathogen or sterile inflammation with an CC (especially chronic) in a tissue, an allergic response in a subject to apathogen or sterile inflammatory disease (e.g. cardiac reperfusion injury, renal reperfusion injury, asthma, thrombosis, CC disease, ulcerative colitis, periodontal disease; also bacterial CC infection, vital infection, parasitic infection, protozoal infection, conditions. The present sequence repersents a gene differentially conditions. The present sequence repersents a gene differentially conditions of the printed specification, but was obtained in the printed specification.
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S 片 S ঠ 밁 밁 δ δ S ঠ 밁 밁 S 밁 밁 문 문 1480 1300 1240 1360 1060 481 421 301 61 1 AGGACGCGGTGGAATGGGCAGCGCTGGAGAGCGAGGTGGCTTCAATAAGCCCTGGTGGACC TCCTGGGGGACCCATGGGTCGCATGGGAGGCCGTGGAGGAGATAGAGGAGGCTTCCCTCC TCCTGGGGGACCCATGGGTCGCATGGGAGGACGCCGTGGAGGAGATAGAGGAGGAGCTTCCCCTCC ACCCCGTGAGGGCAGAGGCATGCCACCACCACTCCGTGGAGGTCCAGGAGGCCCAGGAGG ACTTAAAGTCTCCCTTGCTCGGAAGAAGCCTCCAATGAACAGTATGCGGGGTGGTCTGCC CCCACCCACTGCCAAGGCTGCCGTGGAATGGTTTGATGGGAAAGATTTTCAAGGGAGCAA·1359 CCCACCCACTGCCAAGGCTGCCGTGGAATGGTTTTGATGGGAAAGATTTTCAAGGGAGCAA CATCTACCTGGACAAGGAAACAGGAAAGCCCCAAAGGCGATGCCACAGTGTCCTATGAAGA CATCTACCTGGACAAGGAAACAGGAAAGCCCAAAGGCGATGCCACAGTGTCCTATGAAGA CTTCTTTAAGCAGTGTGGGGTTGTTAAGATGAACAAGAGAACTGGGCAACCCATGATCCA CAACAGTGCAATTTATGTACAAGGATTAAATGACAGTGTGACTCTAGATGATCTGGCAGA CAACAGTGCAATTTATGTACAAGGATTAAATGACAGTGTGACTCTAGATGATGTGGCAGA CATGGATGAAGGACCAGATCTTGATCTAGGCCCTCCTGTAGATCCAGATGAAGACTCTGA CATGGATGAAGGACCAGATCTTGATCTAGGCCCACCTGTAGATCCAGATGAAGACTCTGA AGGACGCGGTGGAATGGGCAGCGCTGGAGAGCGAGGTGGCTTCAATAAGCCTTGGTGGACC ACCCCGTGAGGGCAGAGGCATGCCACCACCTCCGTGGAGGTCCAGGAGGCCCAGGAGG ACTTAAAGTCTCCCTTGCTCGGAAGAAGCCTCCAATGAACAGTATGCGGGGGGGTCTGCC CTTCTTTAAGCAGTGTGGGGTTGTTAAGATGAACAAGAGAACTGGGCAACCCATGATCCA 1539 1479 300 240 1179 180 120 1059 540 1419 1239 1119 60 480

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The invention relates to a method of diagnosing (I progression of benign prostatic hyperplasia (BPH),
                                                                                                                                               Identifying drugs for and diagnosing benign prostatic hyperplasia, by detecting expression levels of one or more genes in prostate cells from patient that are differentially regulated compared to normal prostate
                                                                                                                                                                                                                                                                                                                                                                                                                          07-AUG-2000;
05-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human;
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                                                                       Disclosure; Page 399-400; 444pp; English.
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CC or identifying an agent that modulates the onset or progression of BPH.

CC The method is based on changes in gene expression in BPH tissue isolated

CC from patients exhibiting different clinical states of prostate

CC detecting the expression levels of one or more genes in prostate cells

CC from the subject that are differentially regulated compared to normal

CC prostate cells. (II) comprises preparing a first gene expression profile

CC of BPH cells or BPH-like cell population, exposing the cells to the

CC agent, preparing a second gene expression profile of the agent exposed

CC cells, and comparing the first and second gene expression profiles. (I)

CC is useful for diagnosing the onset or progression of BPH. (II) is useful

CC for identifying an agent that modulates the onset or progression of BPH.

CC or methods are useful to present information identifying the expression

CC expression of gene in the tissue or cells to the level of genes

CC expression level in BPH. Agents using (II) are useful for treating BPH or

CC prostate cancer. ABK64106-ABK64860 represent human benign prostatic

CC hyperplasia gene sequences of the invention
Sequence 2390 BP;
645 A; 589 C; 668 G; 488 T; 0 U; 0 Other;
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Query Match Best Local Sin Matches 1011; 1000 1060 CATGGATGAAGGACCAGATCTTGATCTAGGCCCTCCTGTAGATCCAGATGAAGACTCTGA 61 CAACAGTGCAATTTATGTACAAGGATTAAATGACAGTGTGACTCTAGATGATCTGGCAGA CATGGATGAAGGACCAGATCTTGATCTAGGCCCACCTGTAGATCCAGATGAAGACTCTGA AGGACGCGGTGGAATGGGCAGCGCTGGAGAGCGAGGTGGCTTCAATAAGCCCTGGTGGACC AGGACGCGGTGGAATGGGCAGCGCTGGAGAGCGAGGTGGCTTCAATAAGCCTGGTGGACC Conservative 0 Score 1010.4; DB 6 Pred. No. 7.5e-233; 0; Mismatches 1; Indels 0; Gaps 120 1059 1119 60 180 0

Similarity

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TGGAGACTGGCAGTGTCCCAATCCGGGTTGTGGAAACCAGAACTTCGCCTGGAGAACAGA

AAGAGGACCCCGGGGTTCCCGAGGGAACCCCTCTGGAGGAGGAAACGTCCAGCACCGAGC

TCCTGGGGGACCCATGGGTCGCATGGGAGGCCGTGGAGGAGATAGAGGAGGCTTCCCTCC TCCTGGGGGACCCATGGGTCGCATGGGAGGCCGTGGAGGAGATAGAGGAGGCTTCCCTCC ACCCCGTGAGGGCAGAGGCATGCCACCACCACTCCGTGGAGGTCCAGGAGGCCCAGGAGG

AAGAGGACCCCGGGGTTCCCGAGGGAACCCCTCTGGAGGAAAACGTCCAGCACCGAGC

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ACCCCGTGAGGGCAGAGGCATGCCACCACCACTCCGTGGAGGTCCAGGAGGCCCAGGAGG

1479 480

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RESULT 9
ABN97274
ID ABN9
XX ABN9
AC Gene
KW Gene
KW Gene
KW Meta
KW M
The invention relates to a novel method for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumour in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, involving detecting the level of expression of two or more genes represented in ABN93503-ABN97455 in a tissue sample. The method of the invention has hepatotropic, and cyvostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, drug toxicity, drug efficacy and drug metabolism. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                    Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a patient, involves detecting the level of expression of two or more genes in a liver tissue sample.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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360

1299 300 1239 240 1179 180 1119 120 1059 60 0

420 1359

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1960

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RESULT 10
ACN40903
                                                                              cc mammals. The invention also relates to nucleic acid and polypeptides comprising at least 80% identical to the TAT nucleic acids and polypeptides; expression vectors and host cells comprising a TAT nucleic cc acid; an antibody specific for a TAT polypeptide; applied or organic cc molecule which binds to a TAT polypeptide; applied or organic cc TAT polypeptide; and methods and compositions for the treatment or cd diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, cc antibodies, antagonists, binding molecules and compositions are useful cf or diagnosing or treating a cell proliferative disorder associated with increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder cc cancer, pancreatic cancer, cervical cancer, cancers of the central cc cancer, pancreatic cancer, cervical cancer, cancers of the central cc cancer, pancreatic and lung cancer and gene mapping, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence crepresents a TAT nucleic acid of the invention
Query Match
Best Local Similarity
Matches 1011; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumour-associated antigenic target; TAT; human; overexpression; citumour; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoma; leukaemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to human tumour-associated antigenic target (TAT) polypeptides, and their related nucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACN40903;
                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 5989; 7273pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prostate cancer or tumor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-347921/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wu ID,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-OCT-2002; 2002US-0414971P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-SEP-2003; 2003WO-US028547.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-APR-2004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumour-associated antigenic target (TAT) cDNA DNA269830, SEQ ID NO:5989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACN40903 standard; cDNA; 2390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GETH )
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                                                                              2390
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                              BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhou Y;
                                                                              645
  99.8%; Score 1010.4; DB 13; Length 2390;
99.9%; Pred. No. 7.5e-233;
tive 0; Mismatches 1; Indels 0;
                                                                              A; 589
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                                                                              668 G;
                                                                              488
                                                                              T; 0 U;
                                                                                0 Other;
  Gaps
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	961 TGGAAAAATGGATAAAGGCGAGCACCGTCAGGAGCGCCAGAGATCGGCCCTAC 1012	Qy Db	
960 1959	901 GGGGCCCCCTGGACCTTTGATGGAACAGATGGGAAGAAGAGAGGAGGACGTGGAGGACCC	Qy Db	
900	841 CCGTGGTGGCCGGGGCATGGACCGAGGTGGCTTTGGTGGAGGAAGAAGACGAGGTGGCCCTGG 	ρ <i>δ</i>	
840 1839	781 GGATCGTGGTGGTCCCGGTGGAATGTTCAGAGGTGGCCGTGGTGGAGACAGAGGTGGCTT	g Q	
780 1779	1 GGGTGGTGATCGTGGCAGAGGTGGCCCTGGTGGCATGCGGGGAGGAAGAGGTGGCCTCAT	B 8	
720 1719	61 GTGCAACCAGTGTAAGGCCCCAAAGCCTGAAGGCTTCCTCCCGCCACCCTTTCCGCCCCCCCC	g &	
1659	01 TGGAGACTGGCAGTGTCCCAATCCGGGTTGTGGAAACCAGAACTTCGCCTGGAGAACAGA	B &	
1599	41 AAGAGGACCCCGGGGTTCCCGAGGGAACCCCTCTGGAGGAGGAAACGTCCAGCACCGAGC	g Qy	
540 1539	81 TCCTGGGGGACCCATGGGTCGCATGGGAGGACGAGAGATAGAGGAGGCTTCCCCTCC	유 성	
480 1479	21 ACCCCGTGAGGGCAGAGGCATGCCACCACCACTCGGTGGAGGTCCAGGAGGCCCAGGAGG	B 8	
420 1419	1 ACTTANAGTCTCCCTTGCTCGGAAGAAGCCTCCAATGAACAGTATGCGGGGTGGTCTGCC	g Q	
360 1359	01 CCCACCCACTGCCAAGGCTGCCGTGGAATGGTTTGATGGGAAAGATTTTCAAGGGAGCAA 	B &	
300 1299	41 CATCTACCTGGACAAGGAAACAGGAAAGCCCAAAGGCGATGCCACAGTGTCCTATGAAGA 	B &	
240 1239	81 CTTCTTTAAGCAGTGTGGGGTTGTTAAGATGAACAAGAGAACTGGGCAACCCATGATCCA	B 8	
180 1179	1 CAACAGTGCAATTTATGTACAAGGATTAAATGACAGTGTGACTCTAGATGATCTGGCAGA 	g Qy	
120 1119	61 CATGGATGAAGGACCAGATCTTGATCTAGGCCCACCTGTAGATCCAGATGAAGACTCTGA	B 8	
60 1059	1 AGGACGCGGTGGAATGGGCAGCGCTGGAGAGCGAGGTGGCTTCAATAAGCCTGGTGGACC	D Q	

RESULT 11 ADR07446 ID ADR0744 XX

D ADR07446 standard; cDNA; 2026 BP.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA clones obtained by an oligo-capping method, where none of these clones are identical to any known human mRNAs. The present invention describes an immunoassay to identify agonists and antagonists, as well as antibodies, antisense molecules and siRNAs that can all be used to bind to and modulate expression of the cDNA molecules. As such, these molecules are useful for diagnostic markers or therapeutic targets for the various diseases or morbid states. In particular, they are useful in gene therapy for treating osteoporosis, neurological disease, Alzheimer's disease, Parkinson's disease, dementia, short memory and various cancers, as well as for maintaining equilibrium of sense or motor function, and for treating emotional reaction, fear response and panic. Accordingly, they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian, cytostatic and tranquiliser activities. This polynucleotide is a full length human cDNA sequence of the invention. MOTE: This sequence is not given in the sequence listing of the specification but can be obtained on CD-ROM from the Buropean Patent Office, Vienna Sub-office.
                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Sim
Matches 1010;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Parkinson's disease; dementia; short memory; cancer; sense or motor function; emotional reaction; fear response; osteopathic; neuroprotective; nootropic; antiparkinsonian;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isogai T, Ya
Wakamatsu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-FEB-2003; 2003JP-00102207.
09-MAY-2003; 2003JP-00131452.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New 1995 cDNA, useful
Alzheimer's diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-FEB-2004;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-NOV-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lecules and the encoded proteins thereof. Specifically, it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2004-583265/57
)B; ADR09402.
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porosis; neurological disease; Alzheimer's disease;
                                                                                                                                                                     61
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                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                       2026
                                                                                                                                                 CATGGATGAAGGACCAGATCTTGATCTAGGCCCACCTGTAGATCCAGATGAAGACTCTGA
                                                                                                                                                                                                                                                      AGGACGCGGTGGAATGGGCAGCGCTGGAGAGAGCGAGGTGGCTTCAATAAGCCTGGTGGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 952;
                                                          CAACAGTGCAATTTATGTACAAGGATTAAATGACAGTGTGACTCTAGATGATCTGGCAGA 180
        CAACAGTGCAATTTATGTACAAGGATTAAATGACAGTGTGACTCTAGATGATCTGGCAGA
                                                                                                                                                                                                                          AGGACGCGGTGGAATGGGCAGCGCTGGAGAGCGAGGTGGCTTCAATAAGCCTTGGTGGACC
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A, Ishii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASSOC BIOTECHNOLOGY.
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                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2004EP-00003145
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                                                                                                                                                                                                                                                                                                                                                                                                                                       BP; 540 A; 513 C; 590 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             relates to novel,
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                                                                                                                                                                                                                                                                                                                                                      99.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for treating osteoporosis, neurological diseases, Parkinson's diseases, dementia and various cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nishikawa
Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2686pp; English.
                                                                                                                                                                                                                                                                                                                               0,
                                                                                                                                                                                                                                                                                                                               Score 1008.8; DB 13;
Pred. No. 1.7e-232;
D; Mismatches 2; I
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e R;
                                                                                                                                                                                                                                                                                                                                                                                                                                       383 T; 0 U;
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                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       0 Other;
                                                                                                                                                                                                                                                                                                                                                                                  Length
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                                                                                                                                                                                                                                                                                                                               Gaps
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PRO

cDNA sequence SEQ ID NO:2309.

human; PRO; immune related disease; inflammatory immune response; immune response stimulation; antiallergic; antianaemic; antiarthri antiasthmatic; antidiabetic; antidiabetic; antidiabetic; antidiabetic; antidiabetic; antidiabetic; antityporiatic; antirheumatory; antipporiatic; antirheumatic; antithyroid; CNS; dermatological; gastrointestinal; response; antiarthritic; muscular;

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                                                                                                                                                                                                                                                           The present invention describes an isolated PRO nucleic acid (1). Also Cd described: (1) a vector comprising (1), (2) a host cell comprising the vector of (1); (3) a process for producing a PRO polypeptides; (4) an isolated PRO polypeptide; (5) a chimeric molecule comprising the CC isolated PRO polypeptide; (5) a chimeric molecule comprising the CC polypeptide of (4) fused to a heterologous amino acid sequence; (6) an antibody which specifically binds to a polypeptide of (4); (7) a CC composition of matter comprising a polypeptide of (4), an agonist or CC entragonist of the polypeptide or an antibody that binds to the CC comprising a container, a label on the container and a composition of CC matter of (7); (9) a method of treating an immune related disease in a mammal; (10) a method for determining the presence of a PRO polypeptide CC diagnosing an immune related disease or an inflammatory immune response in mammal; (12) a method of identifying a compound that inhibits or CC mimics the activity of or expression of a gene encoding a PRO polypeptide in mammal; (12) a method of stimulating the immune response in a mammal. The PRO sequences have antiallergic, antianaemic, antiarthritic, antiasthmatic, antithyroid, CNS, dermatological, gastrointestinal, CC antirisementic, antithyroid, CNS, dermatological, gastrointestinal, candidabetic, antithyroid, CNS, dermatological, gastrointestinal, candidabetic, antianaemic, antisprotacic, and conductive, osceopastic, respiratory, vasotropic and curvucide activities, and can be used in gene therapy. The nucleic acid (1) and the encoded polypeptides, compositions, kits and methods are useful in diagnosing and treating an immune related disease and in CC entitulating an immune response. The present sequence represents a human cCC entities and methods are the present sequence and in the encodence from the present invention.
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ACN37537 standard; cDNA; 2177

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18-NOV-2004 (first

Tumour-associated antigenic target (TAT) CDNA DNA323971, SEQ ID NO:490.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC The invention relates to human tumour-associated antigenic target (TAT) CC polypeptides, and their related nucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in C mammals. The invention also relates to nucleic acid and polypeptide sequences at least 80% identical to the TAT nucleic acids and comprising a TAT nucleic acids and polypeptide or organic molecule which binds to a TAT polypeptide; fission proteins comprising a CC malecule which binds to a TAT polypeptide; fission proteins comprising a CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder cancer, pancreatic cancer, cervical cancer, liver cancer, bladder carcous system, melanoma and leukaemia. TAT nucleic acids may further be used as hybridisation probes, in chromosome and gene mapping, in CC chromosome identification and in gene therapy. The present sequence
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                                                                                                                                                                                                                                                                                                     immune deficiency disorder; blood disorder; inflammatory disord infectious disorder; gene therapy; antimicrobial; hepatotropic; immunosuppressive; antirheumatic; ss.
                             (GEMY ) GENETICS INST INC
                                                                        06-APR-2000; 2000US-0195604P
                                                                                                                    29-MAR-2001;
                                                                                                                                                                     18-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                              Human secreted protein; hyperproliferative disorder; autoimmune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA sequence #410 encoding
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The present invention relates to the isolation of novel cDNA sequences which encode human secreted proteins. The cDNA sequences have been concentrated from a variety of human tissues. The invention also provides a comethod for producing proteins from these polymucleotide sequences. The groteins are useful for identifying compounds that modulate their compounds that modulate expression of the polymucleotide sequences of compounds that modulate expression of the polymucleotide sequences compounds that modulate expression of the polymucleotide sequences of the invention are useful for treating diseases such as hyperproliferative disorders (e.g. cancer), immune deficiency disorders (e.g. severe combined immunodeficiency (SCID)), autoimmune disorders (e.g. multiple sclerosis), blood disorders (e.g. thrombocytopaenia), inflammatory disorders (e.g. arthritis) and confectious disorders (e.g. hepatitis). The polymucleotide sequences of the invention are also useful in gene therapy. AASS2214-AASS2338
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K, Graham
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                                                                                                          GGGGCCCCCTGGACCTTTGATGGAACAGATGGGAGGAGGAAGAAGAAGAGAGGACGTGGAGGACC
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Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these

genes.

Ishikawa

Asai

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Takahashi

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Claim

2; Page 794-799;

2690pp;

English.

The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia, occlusive ischaemia or vasospastic ischaemia by measuring expression levels of particular genes (ABI99202 to ABI99912, encoding the the

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protein sequences in ABB57020 to ABB57374) or by determining the expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition-improving drugs or therapeutics for ischaemic diseases. ABI99913 and ABI99914 represent PCR primers for a mouse ischaemic condition related sequence, which are used in the exemplification of the present invention
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                                                                                                       GGATCGTGGTGGTCCCGGTGGAATGTTCAGAGGTGGCCGTGGTGGAGACAGAGGTGGCTT
                                                                                                                                                                                                                                                                    GTGCAACCAGTGTAAGGCCCCAAAGCCTGAAGGCTTCCTCCCGCCACCCTTTCCGCCCCC
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                                                                                GGACCGTGGTGGTCCTGGAGGAATGTTCAGAGGTGGCAGAGGTGGAGACAGAGGAGGCTT
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91.7%;
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Pred. No. 2.7e-201;
0; Mismatches 84;
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Search completed: February 20, 2005, 05:30:50 Job time: 495.802 secs

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Result
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Maximum DB
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Perfect score:
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Listing first 45 s
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

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3: /cgn2_6/ptodata1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata1/ina/backfiles1.seq:*
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US-09-949-016-16785
US-09-949-016-176640
US-09-949-016-176641
US-09-949-016-176631
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Sequence 145, Appli
Sequence 3, Appli
Sequence 31510, A
Sequence 13845, A
Sequence 12371, Ap
Sequence 5928, Ap
Sequence 176640,
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Sequence 5043, Ap
Sequence 5044, Ap
Sequence 13696, A
Sequence 1954, Ap
Sequence 1351, A
Sequence 16785, A
Sequence 16786, A
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Sequence 2, Appli	Sequence 2, Appli	Sequence 10943, A	Sequence 26436, A	Sequence 234, App	Sequence 412, App	•	Sequence 177, App	Séquence 17361, A	Sequence 12147, A	Sequence 30, Appl	Sequence 1, Appli	Sequence 544, App	Sequence 2, Appli	Sequence 4, Appli	Sequence 16775, A	Sequence 14, Appl	Sequence 13765, A

ALIGNMENTS

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Sequence 1, Application Patent No. 5968734
GENERAL INFORMATION:
                                APPLICATION NUMBER: US/08/343,443B
FILING DATE: 18-NOV-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR93/00494
FILING DATE: 19-MAY-1993
PRIOR APPLICATION NUMBER: FR 92/06123
APPLICATION NUMBER: FR 92/06123
APPLICATION NUMBER: FR 92/06123
APPLICATION NUMBER: FR 92/06123
APPLICATION NUMBER: 1992
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J
REGISTRATION NUMBER: 19,763
REGISTRATION NUMBER: 989.6121P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8393
TELEPHONE: 215-875-8393
TELEPAX: 215-875-8394
TELEPAX: 215-875-8394
                      TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Thomas, G.
APPLICANT: Zucman, Jo
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 1910/
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
TO FAXT ed
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APPLICANT:
APPLICANT:
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CORRESPONDENCE ADDRESS:
ADDRESSE: Weiser & Associates
STREET: 230 South Fifteenth Street
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: AEDIT 1.0 DOS text editor
CURRENT APPLICATION DATA:
SEQUENCE CHARACTERISTICS:
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VENTION: NUCLEIC ACID CORRESPONDING TO A GENE OF
VENTION: CHROMOSOME 22 INVOLVED IN RECURRENT CHROMOSOMAL
VENTION: TRANSLATIONS ASSOCIATED WITH THE DEVELOPMENT OF CANCEROUS
VENTION: TUMORS, AND NUCLEIC ACIDS OF FUSION RESULTING FROM SAID
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Peter, Martine
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Desmaze, Chantal
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Thomas, Gilles
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Delattre, Olivier
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Best Local Similarity
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NAME/KEY:
LOCATION:
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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                     CCGTGGTGGCCGGGGCATGGACCGAGGTGGCTTTGGTGGAGGAAGACGAGGTGGCCCTGG 900
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Pred. No. 2.8e-254;
0; Mismatches 1;
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US-09-949-016-5043
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PATENT NO. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 94.5%; Score 956; DB 4; Length Best Local Similarity 100.0%; Pred. No. 4.2e-240; Matches 956; Conservative 0; Mismatches 0; Indel
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GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 5044
LENGTH: 1785
TYPE: DNA
ORGANISM: Human
S-09-949-016-5044
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Best Local Similarity
Matches 956; Conserv
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RESULT 4

US-09-949-016-13696

US-09-949-016-13696, Application US/09949016

; Sequence 13696, Application US/09949016

; Patent No. 6812339
; GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 APPLICANT: VENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001107

CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR APPLICATION NUMBER: 60/237,498
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-10-09
 NUMBER OF SED ID NOS: 207012
 SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 13696
 LENGTH: 6002
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Pred. No. 3.8e-228;
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GENERAL INCOMPATION:
APPLICANT: VENTER, J. Craig et al.
ITILE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSITILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-09-08
UMBER OF SEQ ID NOS: 207012
SOFTWARE: FRANCE (2000-09-08)
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SOFTWARE: FRANCE (2000-09-08)
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                                                                     GAGCTGGAGACTGGCAGTGTCCCAATCCGGGTTGTGGAAACCAGAACTTCGCCTGGAGAA 656
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Pred. No. 5.5e-215;
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US-09-621-976-13361
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SOFTWARE: Patent.pm
SEQ ID NO 13361
LENGTH: 411
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Best Local Similarity
Matches 349; Conserv
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Patent No. 6639063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human
FILE REFERENCE: GENEET: 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
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                                                                                                                                                           ATCCACATCTACCTGGACAAGGAAACAGGAAAGCCCAAAGGCGA-TGCCACAGTGTCCTA 294
                                                                                                                                                                                                                GCAGACTTCTTTAAGCAGTGTGGGGGTTGTTAAGATGAACAAGAGAAACTGGGCAACCCATG
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GAGCAAACTTAAAGTCTCCCTTGCTCGGAAGAAGCCTCCAATGAACAGTA
                                                             TGAAGACCCACCCACTGCCAAGGCTGCCGTGGAATGGTTTGATGGGAAAGATTTTCAAGG
                                                                                            TGAAGACCCACCCACTGCCAAGGCTGCCGTGGAATGGTTTGATGGGAAAGATTTTCAAGG
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US-09-949-016-16786

; Sequence 16786, Application US/09949016
; Patent NO. 6812319
; GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION A:
FILE REFERENCE: CL001307
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/231,758
; PRIOR APPLICATION NUMBER: 60/231,768
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; PRIOR PILING DATE: 2000-10-03
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APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT PILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTMARE: FASSESQ for Windows Version 4.0

SEQ ID NO 16785

LENGTH: 35784

TYPE: DNA
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US-09-949-016-16785
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 16786
LENCTH: 35784
TYPE: DNA
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Best Local S
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hes 268;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTTGGTGGAGGAAGACGAGGTGGCCCTGGGGGCCCCCTGGACCTTTGATGGAACAGATG 33500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGTGGCCGTGGTGGAGACAGAGGTGGCCTTCCGTGGTGGCCGGGGCATGGACCGAGGTGGC
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FILE REFERENCE: CLOOI 307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOSTWARE: FORESEQ for Windows Version 4.0

SEQ ID NO 176641

LENGTH: 601
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US-09-949-016-176641
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Best Local S
Matches 213
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ORGANISM: Human
-09-949-016-176641
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                    Local Similarity
hes 213; Conserv
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181
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                         AGGAGGACGTGGAGGACCTGGAAAAATGGATAA 975
                                                                                               AAGACGAGGTGGCCCTGGGGGGCCCCCTGGACCTTTGATGGAACAGATGGGAAGAAGAAG 942
                                                                                                                                                   TGGAGACAGAGGTGGCTTCCGTGGTGGCCGGGGCATGGACCGAGGTGGCTTTGGTGGAGG 120
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AGGAGGACGTGGAGGACCTGGAAAAATGGATAA 213
                                                                           AAGACGAGGTGGCCCTTGGGGGCCCCCTTGGACCTTTGATGGAACAGATGGGAGGAAGAAG
                                                                                                                                                                                                                              AGGAAGAGGTGGCCTCATGGATCGTGGTGGTCCCCGGTGGAATGTTCAGAGGTGGCCGTGG 60
                                                                                                                                                                                                                                                                                                      21.0%; Score 213; DB 4; 1 ilarity 100.0%; Pred. No. 6.4e-46; Conservative 0; Mismatches 0;
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Pred. No. 5.2e-57;
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Sequence 176664, Application US/09949016

Patent NO. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN G.
TITLE OF INVENTION: WITH HUMAN DISEASE, MET
FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
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US-09-919-039-322
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; ORGANISM: Human
US-09-949-016-176664
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US-09-949-016-176664
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                                                                                  ; NAME/KEY: misc_feature; OTHER INFORMATION: Incyte ID US-09-919-039-322
                                                                                                                                         SOFTWARE: PERL Program
SEQ ID NO 322
LENGTH: 1939
TYPE: DNA
ORGANISM: Homo sapiens
PEATURE:
                                                                                                                                                                                                                                                                                  Sequence 322, Application US/09919039

Patent No. 6727066
GENERAL INFORMATION:
APPLICANT: Kaser, Matthew R.
APPLICANT: Kaser, Matthew R.
TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
FILE REFERENCE: PA-0035 US
CURRENT APPLICATION NUMBER: US/09/919,039
CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 60/222,113
PRIOR APPLICATION NUMBER: 60/222,113
PRIOR FILING DATE: 2000-07-28
Query Match
Best Local Similarity 55.0
Matches 477; Conservative
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Best Local Similarity
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NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASESEQ for Windows Version
                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 401
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                         16.3%;
  Score 164.8; DB 4;
Pred. No. 4.4e-33;
0; Mismatches 297;
                                                                                                       No. 6727066 478620.53
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RESULT 12
US-09-949-016-176637
(Sequence 176637, Application US/09949016
; Sequence 176637, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
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; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.
; SEQ ID NO 176637
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-176637
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US-09-949-016-176638
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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 207012
SOPTWARE: FRATSEQ for Windows
SEQ ID NO 176638
LENGTH: 601
TYPE: DNA
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                                                                                          Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 176638, Application US/09949016 Patent No. 6812339
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Best Local Similarity
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145
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163
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PELICATION NUMBER: 60/237,768
PRIOR PELICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FBSESEQ for Windows Version 4.0
SEQ ID NO 176660
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; ORGANISM: Human
US-09-949-016-176660
                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-176661
                                                                                                                                                                                                                                                                                                        FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                              Query Match
Best Local Similarity
Matches 137; Conserv
                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 176661
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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Best Local Similarity
Matches 137; Conserv
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                                                                                 13.4%; Score 135.8; DB 4;
larity 98.6%; Pred. No. 1e-25;
Conservative 0; Mismatches 2;
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Search completed: February 20, 2005, 16:33:17 Job time: 177.828 secs

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Database
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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1012
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11231.185 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/pCT_NEW_PUB.seq:*
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gn2 6/ptodata/2/pubpna/US09B PUBCOMB.seq:*
gn2 6/ptodata/2/pubpna/US09C PUBCOMB.seq:*
gn2 6/ptodata/2/pubpna/US09C PUBCOMB.seq:*
gn2 6/ptodata/2/pubpna/US10A PUBCOMB.seq:*
gn2 6/ptodata/2/pubpna/US10B PUBCOMB.seq:*
gn2 6/ptodata/2/pubpna/US10C PUBCOMB.seq:*
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/pubpna/US06_NEW_PUB.seq:*
/pubpna/US06_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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570 508.4 437.2 309	1012 1010.4 1010.4 1010.4 882.4	1012	Score
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14 US-10-198-846-9847 10 US-09-918-995-27690 10 US-09-918-995-9557 9 US-09-925-301-669	18 US-10-791-017A-1 9 US-09-880-107-3769 10 US-09-960-706-1081 10 US-09-873-319-717 9 US-09-822-830A-410	US-10-094-749-1074 US-09-822-830A-49	SUMMARIES
Sequence 9847, Ap Sequence 27690, A Sequence 9557, Ap Sequence 669, App	Sequence 1, Appli Sequence 3769, Ap Sequence 1081, Ap Sequence 717, App Sequence 410, App	Sequence 1074, Ap Sequence 49, Appl	Description

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	6.5	6.7	6.7	6.7	7.1	7.1	7.3 1	7.5	7.5	7.7	7.9	7.9	7.9	8.1	8. ₃	8.4	8.9	9.0	9.9			11.0	11.0	13.0	15.2	16.3	16.3	16.3	21.0	25.0	25.1	25.5	25.5	26.7
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*	US-10-029-386-20241	-10-437-963-	US-10-292-798-1629	US-10-017-161-1981	US-10-424-599-44846	US-09-918-995-23349	US-10-148-806-3	US-10-425-115-42131	US-10-425-114-4694	US-10-029-386-20388	-10-425-115-	US-10-425-114-31980	US-10-767-701-1751	US-10-437-963-89443	US-10-425-115-42135	US-10-198-846-7976	US-09-933-797-351	US-10-739-930-501	US-09-918-995-27342	US-10-101-510-297	US-10-144-649A-145	US-09-854-133-145	US-09-738-973-145	US-09-918-995-2865	US-09-918-995-19709	US-09-919-039-322	US-10-439-703-58	US-10-755-889-649	US-10-469-285-488	US-09-864-761-25438	US-10-029-386-18163	US-10-029-386-4463	US-09-864-761-8728	US-09-960-352-3851
	20241,	3998,	1629,	1981, 2				Sequence 42131, A		20388,		31980,	1751,	89443,	421	Sequence 7976, Ap	351, ,	501	27	297,	e 145		145, Ar			Sequence 322, App		649,		25438	1816	e 4463	872	Sequence 3851, Ap

ALIGNMENTS

RESULT 1
US-10-094-749-1074
; Sequence 1074, Application US/10094749
; Publication No. US20030219741A1 APPLICANT: SEKI, MACHIKO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OSHIKAWA, TSUTOMU
APPLICANT: WAGAHARI, KENNI
APPLICANT: WAGAHARI, KENNI
APPLICANT: WASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR FILING DATE: 2002-03-12
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: 57
PRIOR APPLICATION NUMBER: 57
PRIOR APPLICATION NUMBER: 381
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PSEC ID NOS: 3381
SOFTWARE: PSEC ID NOS: 3381 SEQ ID NO.1074 . APPLICANT: PPLICANT: INFORMATION: OTSÚKA, KAORU NAGAI, KEIICHI IRIE, RYOTARO TAMECHIKA, ICHIRO SUGIYAMA, TOMOYA OTSUKI, TETSUJI WAKAMATSU, AI SATO, HIROYUKI AMAMOTO, JUN-ICHI SONO, YUUKO YURI SHIZUKO TAKAO TOMOYASU

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; TYPE: DNA
; ORGANISM: Homo sapiens
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                                                                    CCGTGGTGGCCGGGGCATGGACCGAGGTGGCTTTGGTGGAGGAAGACGAGGTGGCCCTGG
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CURRENT FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/195,604
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 631
SOFTWARE: PALENTIN VOT. 2.0
SEQ ID NO 49
LENGTH: 2176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 1012; DB 9; Best Local Similarity 100.0%; Pred. No. 1.5e-283; Matches 1012; Conservative 0; Mismatches 0;
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APPLICANT: Wong, Gordon G.
APPLICANT: Clark, Hilary
APPLICANT: Clark, Hilary
APPLICANT: Pechtel, Kim
APPLICANT: Agostino, Michael J.
APPLICANT: Howes, Steven H.
APPLICANT: Resnick, Richard J.
APPLICANT: Gulukota, Kamalakar
APPLICANT: Gulukota, Kamalakar
APPLICANT: Graham, James R.
TITLE OF INVENTION: POLYMUCIEOTIDES ENCODING NOVEL SECRETED PROTEINS
FILE REFERENCE: GIN 6402
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ORGANISM: Homo sapiens
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Sequence 1, Application US/10791017A

Publication No. US20040197827A1

GENERAL INFORMATION:
APPLICANT: JENAPHARM GmbH & Co. KG

TITLE OF INVENTION: Methods for Determining Hor
FILE REFERENCE: Pat 3684/11

CURRENT APPLICATION NUMBER: US/10/791,017A

CURRENT FILING DATE: 2004-03-02

NUMBER OF SEQ ID NOS: 7

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 1

SEQ ID NO 1

LENGTH: 2390

TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (44) . (2011)

OTHER INFORMATION: EWS

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Matches 1012; Conservative 0
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Pred. No. 1.6e-283;
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US-09-880-107-3769
/ Sequence 3769, Application US/09880107
/ Patent No. US20020142981A1
/ GENERAL INFORMATION:
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APPLICANT: Horne, Darci T.

APPLICANT: Vockley, Joseph G.

APPLICANT: Scherf, Uwe

APPLICANT: Gene Logic, Inc.

TITLE OF INVENTION: Gene Expression Profiles in FILE REFERENCE: 44921-5028-WO

CURRENT APPLICATION NUMBER: US/09/880,107

CURRENT FILING DATE: 2001-06-14

PRIOR APPLICATION NUMBER: US 60/211,379

PRIOR APPLICATION NUMBER: US 60/237,054

PRIOR FILING DATE: 2000-10-02

NUMBER OF SEQ ID NOS: 3950
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3769
; LENGTH: 2390
; TYPE: DNA
; ORGANISM: Homo saplens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No US-09-880-107-3769
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CCGTGGTGGCCGGGCATGGACCGAGGTGGCTTTGGTGGAGGAAGACGAGGTGGCCCTGG 1899
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QY 481 TCCTGGGGGACCCA Db 1480 TCCTGGGGGACCCA	Oy 421 ACCCCGTGAGGGCA	1300 361 1360	181 1180 241 1240	Qy 61 CATGGATGAAGGAC Db 1060 CATGGATGAAGGAC Qy 121 CAACAGTGCAATTT Db 1120 CAACAGTGCAATTTT	Qy 1 AGGACGCGGTGGAA' Db 1000 AGGACGCGGTGGAA'	Query Match 99.8%; Best Local Similarity 99.9%; Matches 1011; Conservative	RESULT 5 US-09-060-706-1081 US-09-960-706-1081, Application US/09960706 publication No. US20030134280A1 GENERAL INFORMATION: APPLICATT: Munger, William E. TITLE OF INVENTION: Identifying Drugs fo: TITLE OF INVENTION: Gene Expression Proi FILE REFERENCE: 44921-5029-01US CURRENT APPLICATION NUMBER: US/09/960,700 CURRENT FILING DATE: 2001-09-24 PRIOR FILING DATE: 2001-09-24 PRIOR FILING DATE: 2001-09-27 PRIOR FILING DATE: 2001-06-07 PRIOR FILING DATE: 2001-06-07 PRIOR FILING DATE: 2001-06-07 PRIOR FILING DATE: 2001-06-05 NUMBER OF SEQ ID NOS: 1124 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 1081 LENGTH: 2390 TYPE: DNA ORGANISM: Homo sapiens FEATURE: OTHER INFORMATION: Genbank Accession No US-09-960-706-1081	Qy 901 GGGGCCCCTGGACC Db 1900 GGGGCCCCCTGGACC Qy 961 TGGAAAAATGGATAA Db 1960 TGGAAAAATGGATAA
TCCTGGGGGACCCATGGGTCGCATGGGAGGACGAGGAGAGAGA	ACTIMAMSTETICECTISCITEMAMSMASCLICEMATIMACASTA ISCUSSOTOS IC SECONDES ACTIONS A	CCCACCACTECCAAGECTECCAAGECTECCAATGATTGATTGATGGAAAAAATTTTCAAGGGAGCAA	CTTCTTTAGCAGTGTGGGGTTGTTAAGATGAACAAGAGAACTGGGCAACCCATGATCCA [CATGGATGAAGGACCAGATCTTGATCTAGGCCCACCTGTAGATCCAGATGAAGACTCTGA [AGGACGCGGTGGAATGGGCAGCGCTGGAGAGCGAGGTGGCTTCAATAAGCCTGGTGGACC 	.8%; Score 1010.4; DB 10; Length 2390; .9%; Pred. No. 4.6e-283; e 0; Mismatches 1; Indels 0; Gaps	r and Diagnosis of Eiles	GGGGCCCCCTGGACCTTTGATGGAACAGATGGGAGGAAGAAGAGGAGGACGTGGAGGACCGTGGAGGACCGTGGAGGACCGTGGAGGACCGTGGAGGACCGTGGAGGACCGTGGAGGACCCCCCTGGACCTTTGATGGAACAGATGGGAGGAAGAAGAAGAAGAAGAAGACGTCAGGACCCTAC 1012 TGGAAAAATGGATAAAGGCGAGCACCGTCAGGAGCGCAGAGATCGGCCCTAC 2011 TGGAAAAATGGATAAAGGCGAGCGACCGTCAGGAGCGCAGAGATCGGCCCTAC 2011
C 540	480	A 1359 A 1359 C 420 C 1419	12 30 24		c 60 c 1059	0;	Benign Prostatic Hyperpla:	1959

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Sequence 717, Application US/09873319A
Publication No. US20030134324A1
GENERAL INFORMATION:
APPLICANT: Munger, William E.
APPLICANT: Kulkarni, Prakash
APPLICANT: Kulkarni, Prakash
APPLICANT: Waga, Iwao
APPLICANT: Yamamoto, Jun
TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic
TITLE OF INVENTION: Hyperplasia Using Gene Expression Profiles
FILE REFERENCE: 44921-5029-US
CURRENT APPLICATION NUMBER: US/09/873,319A
CURRENT APPLICATION NUMBER: US/09/873,319A
CURRENT APPLICATION NUMBER: US/09/873,319A
CURRENT FILING DATE: 2001-06-05
EARLIER APPLICATION NUMBER: US/09/873,323
EARLIER FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 755
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 717
LENGTH: 2390
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
FEATURE:
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US-09-873-319-717
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RESULT 7

US-09-822-830A-410/c

US-09-822-830A-410/c

Sequence 410, Application US/09822830A

Patent No. US20020142952A1

GENERAL INFORMATION:

APPLICANT: Genetics Institute, Inc.

APPLICANT: Wong, Gordon G.

APPLICANT: Clark, Hilary

APPLICANT: Clark, Hilary

APPLICANT: Agostino, Michael J.

APPLICANT: Howes, Steven H.

APPLICANT: Resnick, Richard J.
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APPLICANT: Graham, James R.,
FITTE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
FILE REFERENCE: GIN 6402
CURRENT APPLICATION NUMBER: US/09/822,830A
CURRENT FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/195,604
PRIOR PILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 631
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 410
LENGTH: 2273
TYPE: DNA
ORGANISM: Homo sapiens
US-09-822-830A-410
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                                            TGGAGACTGGCAGTGTCCCAATCCGGGTTGTGGAAACCAGAACTTCGCCTGGAGAACAGA
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GGATCGTGGTGGTCCCGGTGGAATGTTCAGAGGTGGCCGTGGTGGAGACAGAGGTGGCTT 840
                                                                                                                  GTGCAACCAGTGTAAGGCCCCAAAGCCTGAAGGCTTCCTCCCGCCACCCTTTCCGCCCCC
                                                                                                                                              TGGAGACTGGCAGTGTCCCAATCCGGGTTGTGGAAACCAGAACTTCGCCTGGAGAACAGA
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94.6%;
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Pred. No. 7.5e-246;
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FILE REFERENCE: MRI-049
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9847
LENGTH: 2299
TYPE: DNA
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US-10-198-846-9847
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Matches
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Best Local &
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APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youngyao
APPLICANT: Wang, Youngyao
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS,
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT,
TITLE OF INVENTION: THERAPY OF BREAST CANCER
 1432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tch 56.3%; Score 570; DB 14; al Similarity 100.0%; Pred. No. 5.3e-155; 570; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                               56 GGACCCATGGATGAAGGACCAGATCTTGATCTAGGCCCACCTGTAGATCCAGATGAAGAC
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                                                                                                                                                                        GAAGACCCACCCACTGCCAAGGCTGCCGTGGAATGGTTTGATGGGAAAGATTTTCAAGGG
                                                                                                                                                                                                           ATCCACATCTACCTGGACAAGGAAACAGGAAAGCCCCAAAGGCGATGCCACAGTGTCCTAT
                                                                                                                                                                                                                                ATCCACATCTACCTGGACAAGGAAACAGGAAAGCCCCAAAGGCGATGCCACAGTGTCCTAT
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                                  CTGCCACCCCGTGAGGGCAGAGGCATGCCACCACCACTCCGTGGAGGTCCAGGAGGCCCA 475
                                                                                                                                         GAAGACCCACCGACTGCCAAGGCTGCCGTGGAATGGTTTGATGGGAAAGATTTTCAAGGG
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Sequence 27690, Application US/09918995

Publication No. US20030073623A1

GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBT
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
FRIOR APPLICATION NUMBER: US/09/235,076
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTMARE: FastcSEQ for Windows Version 3.0
SEQ ID NO 27690
LENCTH: 550
TYPE: DNA
ORGANISM: Homo.sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(550)
UTHER INFORMATION: n = A,T,C or G
US-09-018-095-27690
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Best Local Similarity 97.5%;
Matches 515; Conservative
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                     ATGCGGGGAGGAAGAGGTGGCCTCATGGATCGTGGTGGTCCCGGTGGAATGTTCAGAGGT
                                                                               TTCCTCCCGCCACCCTTTCCGCCCCCGGGTGGTGATCGTGGCAGAGGTGGCCCTGGTGGC
                                                                                                                                              AACCAGAACTTCGCCTGGAGAACAGAGTGCAACCAGTGTAAGGCCCCAAAGCCTGAAGGC
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                                                              TTCCTCCCGCCACCCTTTCCGCCCCCGGGTGGTGATCGTGGCAGAGGTGGCCCTGGTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 508.4; DB 10; Length Pred. No. 2.6e-137;
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                                           RESULT 11
US-09-925-301-669
Sequence 669, Application US/09925301 Patent No. US20020052308A1 GENERAL INFORMATION:
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LENGTH: 568
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(568)
; OTHER INFORMATION: n = A,T,C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Hyseq, Inc.
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUE
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRA
FILE REFERENCE: 2041-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR PILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FASESEQ for Windows Version 3.0
SEQ ID NO 9557
LENGTH: 568
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US-09-918-995-9557
; Sequence 9557, Application No. US200:
; Publication No. US200:
; GENERAL INFORMATION:
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Best Local Similarity 97.5
Matches 466; Conservative
510
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ACCCCGTGAGGGCAGAGCCACCACCACCTTTCGTGAGGTCCAGGAGGCCCCAGA 567
                 ACCCCGTGAGGGCAGAGGCATGCCACCACCACCCCGTGGAGGTCCAGGAGGCCCCAGGA 478
                                                                                 ACTTAAAGTCTCCCCTTGCTCGGAAGAAGCCTCCAATGAACAGTATGCGGGGTGGTCTGCC 420
                                                                                                                            CCCACCCACTGCCAAGGCTGCCGTGGAATGGTTTGATGGGAAAGATTTTCAAGGGAGCAA 450
                                                                                                                                                   CCCACCCACTGCCAAGGCTGCCGTGGAATGGTTTTGATGGGGAAAGATTTTTCAAGGGAGCAA 360
                                                                                                                                                                                                CATCTACCTGGACAAGGAAACAGGAAAGCCCAAAGGCGATGCCACAGTGTCCTATGAAGA
                                                                                                                                                                                                                             CATCTACCTGGACAAGGAAACAGGAAAGCCCCAAAGGCGATGCCACAGTGTCCTATGAAGA 300
                                                                                                                                                                                                                                                              CTTCTTTAAGCAGTGTGGGGTTGTTAAGATGAACAAGAGAACTGGGCAACCCATGATCCA
                                                                                                                                                                                                                                                                                                 CTTCTTTAAGCAGTGTGGGGTTGTTAAGATGAACAAGAGAACTGGGCAACCCATGATCCA
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                                                                ACTTANAGTCTCCCTTGCTCGGAAGAAGCCTTCCAATGAACAGTATGC-GGGTGGGCTGCC
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LIBRARIES
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Acids, Proteins

and Antibodies

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CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT PILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 669
LENGTH: 545
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Best Local
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TITLE OF INVENTION: Nucleic
FILE REFERENCE: PA106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
LOCATION: (337)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
LOCATION: (453)
OTHER INFORMATION: n equals a,t,g,
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LOCATION: (13)
OTHER INFORMATION: n equals
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LOCATION: (11)
OTHER INFORMATION: n equals
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LOCATION: (58)
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hes 396; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGAGGCCCAGGAGGTCCTGGGGGACCCCATGGGTCGCATGGGAGGCCCGTGGAGGAGATAGA 526
GGACGTGGAGGACCTGGAAAAA 968
                                                              CGAGGTGGCCCTGGGGGCCCCCTGGACCTTTGATGGAACAGATGGGAGGAAGAAGAAGAGA
                                                                                                                                          GACAGAGGTGGCTTCCGTGGTGGCCGGGGCATGGACCGAGGTGGCTTTGGTGGAGGAAGA
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                                                                                                                                                                                                                                                                                                                                                                GATTTCTGCTGTGATGTAATTGTATGCAGGGGTTGTGGAAACCAGAACTTCGCCTGGAGA 284
                                                                                                                                                                                                                                                                                                                                                                                                        GCCTGGAGAACAGAGTGCAACCAGTGTAAGGCCCCAAAGCCTGAAGGCTTCCTCCCGCCA 706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GNCGGCCGCTCTAGAACTAGTGGATCCCCCGGGCTGCAGGAATTCGGCACGAGAGATAGA
                                                                                                                     GACAGAGGTGGCTTCCGTGGTGGCCGGGGCATGGACCGAGGTGGCTTTNGTGGAGGAAGA
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Pred. No. 2.5e-79;
0; Mismatches 93
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; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 17-LIB3057-024-Q1-K1-E1
US-09-960-352-3851
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US-09-864-761-8728
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                                                                                                                                                                Sequence 8728, Application US/09864761 Patent No. US20020048763A1 GENERAL INFORMATION:
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LENGTH: 361
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Best Local Similarity
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APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
APPLICANT: Mathialagan, Nagappan
TITLE OP INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OP INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILLING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FILE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     197 GGGGTTGTTAAGATGAACAAGAGAACTGGGCAACCCATGATCCACATCTACCTGGACAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 TAAACAGGAAAGCCCAAAGGCGATGCTACGGTGTCTTACGAAGACCCAGCAACTGCCAAA
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Pred. No. 5.5e
0; Mismatches
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Best Local Similarity
Matches 268; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOPTWARE: Annomax Sequence Listing SEQ ID NO 8728 LENGTH: 503
                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: M
OTHER INFORMATION: E
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NUMBER OF SEQ ID NOS: 49117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              c FILING DATE: 2000-09-21
APPLICATION NUMBER: US 09/608;408
FILING DATE: 2000-06-30
APPLICATION NUMBER: US 09/774,203
FILING DATE: 2001-01-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 2001-01-30
APPLICATION NUMBER: US 60/234,687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US01/00662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00669
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US01/00666 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: GB 24263.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 60/207,456 FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/180,312 FILING DATE: 2000-02-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US01/00670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US01/00663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US01/00665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US01/00667
                                                                                                                                                                                                                                                                                                                                                      INFORMATION:
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                                                                                                                                                                                                                      GGCTTCCCGCCACCCTTTCCGCCCCCGGGTGGTGATCGTGGCAGAGGTGGCCCTGGT
                                                                                                GGTGGCCGTGGTGGAGACAGAGGTGGCTTCCGTGGTGGCCGGGGCATGGACCGAGGTGGC
                                                                                                                                                                                                 GACTGCTTTCGCCCTGCTATTCTCACCTTAGGTGGTGATCGTGGCAGAGGTGGCCCTGGT
                            TTTGGTGGAGGAAGACGAGGTGGCCCTGGGGGCCCCCTGGACCTTTGATGGAACAGATG 931
                                                                                                                                GGCATGCGGGGAGGAAGAGGTGGCCTCATGGATCGTGGTGCTCCCGGTGGAATGTTCAGA
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EXPRESSED IN PLACES
EXPRESSED IN HEART,
EXPRESSED IN FETAL
EXPRESSED IN HELA,
EXPRESSED IN BONE N
EXPRESSED IN LUNG,
EXPRESSED IN ADULT
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NUMBER: US 09/632,366
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ID IN HEART, SIGNAL = 2.3

ID IN FETAL LIVER, SIGNAL = 2.5

ID IN HELA, SIGNAL = 2.5

ID IN BONE MARROW, SIGNAL = 3.5

ID IN LUNG, SIGNAL = 5.8

ID IN ADULT LIVER, SIGNAL = 1.7
                                                                                                                                                                                                                                                                    <u>,</u>
                                                                                                                                                                                                                                                                Score 258.4; DB 9
Pred. No. 1.3e-64;
0; Mismatches 16
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RESULT 15
US-10-029-386-18163/c
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzal, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SII
TITLE OF INVENTION: EXPRESSION ANALYSIS TW:
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
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US-10-029-386-4463/c
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                                                                                                                                                                       Sequence 18163, Application US/10029386 Publication No. US20030194704A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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Best Local :
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: HANZEL, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: ABOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT APPLICATION DATE: 2001-12-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: MAP TO CHR22.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.6
OTHER INFORMATION: SWISSPROT HIT: P18713, EVALUE 1.20e+00
OTHER INFORMATION: EST HUMAN HIT: BE897260.1, EVALUE 0.00e
OTHER INFORMATION: NT HIT: Y07848.1, EVALUE 0.00e+00
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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< Local 5_
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGAGGAAGAAGAGGAGGACGTGGAGGACCTTGGAAAAAATGGATAA
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Pred. No. 1.3e-64;
O; Mismatches 16;
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Search completed: February 20, 2005, 22:47:58 Job time: 534.573 secs
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OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.6
OTHER INFORMATION: SWISSPROT HIT: Q07050, EVALUE 2.00e+00
OTHER INFORMATION: NT HIT: X73003.1, EVALUE 0.00e+00
OTHER INFORMATION: EST_HUMAN.HIT: BE897250.1, EVALUE 0.00e+00
US-10-029-386-18163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 18163
LENGTH: 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 25.1%;
Best Local Similarity 98.8%;
Matches 256; Conservative
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                                                                        GACCTGGAAAAATGGATAA 975
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                                                                                                                                                                                                                                                GCTTCCGTGGTGGCCGGGGCATGGACCGAGGTGGCTTTGGTGGAGGAAGACGAGGTGGCC 896
                                                                                                                                                                                                                                                                                                                       TCATGGATCGTGGTGGTCCCGGTGGAATGTTCAGAGGTGGCCGTGGTGGAGACAGAGGTG 836
                                                                                                                                                                                                                           GCTTCCGTGGTGGCCGGGCATGGACCGAGGTGGCTTTGGTGGAGGAAGACGAGGTGGCC
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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792.8
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length: 2000000000
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Gapop 10.0 , Gapext 1.0
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12886.762 Million cell updates/sec
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9b est4:2
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9b est4:3
9b est5:3
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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ALIGNMENTS

REFERENCE AUTHORS ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 1 CR593724 ORIGIN FEATURES REFERENCE DEFINITION COMMENT rocus TITLE JOURNAL TITLE JOURNAL REMARK Query Match Best Local Similarity Matches 1012; Conserv AUTHORS source Direct Submission Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage: Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage: BP 191 91006 EVRY cedex - FRANCE (B-mail: seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr) let strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2073) Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length CDNA libraries and normalization Unpublished Faraday Avenue 2 (bases 1 to 2073) Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Homo sapiens (human) CR593724.1 GI:50474531 HTC; CNSLT_CDNA. CR593724 2073 bp mRNA linear full-length cDNA clone CS0DI011YO05 of Placenta Cot of Homo sapiens (human). CR593724 Genoscope. /organism="Homo sapiens" /mol type="mRNA" /db_xref="taxon:9606" /clone="CSODIO11Y005" /tissue_type="Placenta Cot 25 /plasmid="pCWVSPORT_6" location/Qualifiers . .2073 100.0%; Score 1012; DB 3 100.0%; Pred. No. 8e-241; tive 0; Mismatches 0 DB 3; 25-normalized" Length HTC 21-JUL-2004 25-normalized

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Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2083)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished
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1st strand cDNA was primed with a NotI-oligo(dT) primer. Five end enriched, double-strand cDNA was digested with Not I and into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Lik was normalized. Library was constructed by Life Technologies, division of Invitrogen.

Location/Qualifiers
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Submitted (20-JUL-2004) Genoscope - Centre
BP 191 91006 EVRY cedex - FRANCE (E-mail:
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/clone="CSODG004YL23"
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gource Origin	FEATURES	COMMENT	REFERENCE AUTHORS TITLE JOURNAL	JOURNAL REMARK	REFERENCE AUTHORS TITLE	KEYWORDS SOURCE ORGANISM	DEFINITION ACCESSION VERSION	RESULT 3 CR619493	B 8	B 8	B &	g Qy	D Qy	g Qy	DB QY	D Q
	into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. Location/Qualifiers		2 (bases 1 to 2103) 2 (bases 1 to 2103) Genoscope. Direct Submitsion Direct Submitsion Submitted (20-JIII-2004) Genoscope - Centre National de Semiencare	Unpublished Contact : Feng Liang Email : I http://fulllength.invitrogen.c	Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2103) 5 Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization	HTC; CNSIT CNA. HTM (C) CNSIT CNA. Homo sapiens (human) Homo sapiens Eukaryota Metazoa Chordata.	full-length cDNA clone CSODIO76YO2: of Homo mapiens (human). CR619493 CR619493 1 GT:SDSDORGO	CR619493 2103 bp mRNA linear	961 TGGAAAAATGGATAAAGGCGAGCACCGTCAGGAGCGCAGAGATCCGCCCTAC 1012 	901 GGGGCCCCTGGACCTTTGATGGAACAGATGGGAAGAAGAAGAGAGGACGTGGAGGACC 960 	841 CCGTGGTGGCCGGGGCATGGACCGAGGTGGCTTTGGTGGAGGAAGACGAAGTGGCCCTGG 900	781 GGATCGTGGTCCCGGTGGAATGTTCAGAGGTGGCCGTGGTGGAGACAGAGGTGGCTT 840	721 GGGTGGTGATCGTGGCAGAGGTGGCCCTGGTGGCATGCGGGGAGGAAGAGGTGGCCTCAT 780	661 GTGCAACCAGTGTAAGGCCCCAAAGCCTGAAGGCTTCCTCCCGCCACCCTTTCCGCCCCC 720	601 TGGAGACTGGCAGTGTCCCAATCCGGGTTGTGGAAACCAGAACTTCGCCTGGAGAACAGA 660 	541 AAGAGGACCCCGGGGTTCCCGAGGGAACCCCTCTGGAGGAAGGA
B & B &	Db Qy	B &	B &	₽ Q	B &	당 왕	유 성	B &	₽ <i>Q</i>	B &	₽ Q	B 8	B &	B &	B 8	Query Ma Best Loc Matches
901 GGGGCCCCTGGACCTTGATGGAACAGATGGGAAGAAGAAGAAGAAGAAGACGTGGAGGACCT 	841 CCGTGGTGGCCGGGGCATGGACCGAGGTGGCTTTGGTGGAGGAAGACGAGGTGGCCCTGG	781 GGATCGTGGTGGTCCCGGTGGAATGTTCAGAGGTGGCCGTGGTGGAGACAGAGGTGGCTT 	721 GGGTGGTGATCGTGGCAGAGGTGGCCCTGGTGGCATGCGGGGAGGAAGAGGTGGCCTCAT	661 GTGCAACCAGTGTAAGGCCCCAAAGCCTGAAGGCTTCCTCCCGCCACCCTTTCCGCCCC	601 TGGAGACTGGCAGTGTCCCAATCCGGGTTGTGGAAAACCAGAACTTCGCCTGGAGAACAG. 	541 AAGAGGACCCCGGGGTTCCCCGAGGGAACCCCTCTGGAGGAAGGA	481 TCCTGGGGGACCCATGGGTCGCATGGGAGGCCGTGGAGGAGATAGAGGAGGCTTCCCTC	421 ACCCCGTGAGGGCAGAGGCATGCCACCACTCCGTGGAGGTCCAGGAGGCCCAGGAGGG	361 ACTTANAGTCTCCCTTGCTCGGAAGAAGCCTCCAATGAACAGTATGCGGGGTGGTCTG	301 CCCACCCACTGCCAAGGCTGCCGTGGAATGGTTTGATGGGAAAGATTTTCAAGGGAGCAA 	241 CATCTACCTGGACAAGGAAACAGGAAAGCCCAAAGGCGATGCCACAGTGTCCTATGAAGA 	181 CTTCTTTAAGCAGTGTGGGGTTGTTAAGATGAACAAGAGAACTGGGCAACCCATGATCCA	121 CAACAGTGCAATTTATGTACAAGGATTAAATGACAGTGTGACTCTAGATGATCTGGCAGA 	61 CATGGATGAAGGACCAGATCTTGATCTAGGCCCACCTGTAGATCCAGATGAAGACTCTGA	1 ACGACGCGGTGGAATGGGCAGCGCTGGAGAGCGACGTGGCTTCAATAAGCCTGGTGGACC	y Match 100.0%; Score 1012; DB 3; Length 2103; Local Similarity 100.0%; Pred. No. 8.1e-241; hes 1012; Conservative 0; Mismatches 0; Indels 0; Gaps

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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2157)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished
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1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a
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HTC; CNSLT_CDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation
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                                                                                                              CCCACCCACTGCCAAGGCTGCCGTGGAATGGTTTGATGGGAAAGATTTTCAAGGGAGCAA 360
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                                               ACTTAAAGTCTCCCTTGCTCGGAAGAAGCCTCCAATGAACAGTATGCGGGGTGGTCTGCC 420
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/mol type="mRNA"
/db_xref="taxon:9606"
/clone="CSODIO10YII2"
/tissue_type="Placenta Cot
/plasmid="pCMVSPORT_6"
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ative 0;
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Pred. No. 8.1e-241;
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                                                                                                                     Submitted (20-JUL-2004) Genoscope - Centre National de Sequencag
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five pr
                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2314)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization
                                      end enriched, double-strand cDNA was digested with Not I and cinto the Not I and EcoR V sites of the pCMVSPORT 6 vector. Likwas normalized. Library was constructed by Life Technologies, division of Invitrogen.
                                                                                                                                                                                                                                                                                        Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CR608375.1 GI:50489182
                                                                                                                                                                                                                                                                                                                               Unpublished
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6 vector. Library
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/organism="Homo sapiens"

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GGGGCCCCCTGGACCTTTGATGGAACAGATGGGAAGAAGAAGAAGAGGAGGACGTGGAAGAACC
                                                  CCGTGGTGGCCGGGGCATGGACCGAGGTGGCTTTGGTGGAGGAGGAAGACGAGGTGGCCCTGG
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/db xref="taxon:9606"
/db xref="taxon:9606"
/clone="CSODI039YJZ4"
/tissue_type="Placenta Cot
/plasmid="pCMVSPORT_6"
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Local Similarity
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1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2070)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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HTC; CNSLT cDNA.
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSOD1068YN23"
/tissue_type="Placenta Cot 2
/plasmid="pCMVSPORT_6"
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Pred. No. 7.8e-237;
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full-length cDNA clone
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                                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Verte
Eukaryota; Metazoa; Chordata; Catarrhini; Hon
Mammalia; Eutheria; Primates; Catarrhini; Hon
1 (bases 1 to 2093)
Li,W.B.; Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
                                                                 Genoscope.
                                                                            Faraday Avenue
2 (bases 1 to 2093)
                                                                                                   Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation
                                                                                                                                                                                                                                of Homo sapiens (human)
CR594868
CR594868.1 GI:50475675
HTC; CNSLT_CDNA.
                                                   Direct Submission
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TGGAGACTGGCAGTGTCCCAATCCGGGTTGTGGAAACCAGAACTTCGCCTGGAGAACAGA
                      TGGAGACTGGCAGTGTCCCAATCCGGGTTGTGGAAACCAGAACTTCGCCTGGAGAACAGA
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/mol type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI064YE15"
/tissue_type="placenta Cot 2
/plasmid="pCMVSPORT_6"
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Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and Ecok V sites of the pcwvSpORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation
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Mammalia; Eutheria; Primates;
1 (Dases 1 to 2126)
Li,W.B., Gruber,C., Jessee,J.
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                  CTTCTTTAAGCAGTGTGGGGTTGTTAAGATGAACAAGAGAACTGGGCAACCCATGATCCA
                                                                              CAACAGTGCAATTTATGTACAAGGATTAAATGACAGTGTGACTCTAGATGATCTGGCAGA
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                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db xref="taxon:9606"
/clone="CSODF037VIO7"
/tisue_type="Fetal brain"
/plasmid="pCMVSPORT_6"
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Location/Qualifiers
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                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2159)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Pull-length cDNA libraries and normalization
Unpublished
                                                                                                                                                                                         (human).
CR625247
             Contact : Feng Liang Email : fliang@lifetech.
http://fulllength.invitrogen.com/ InVitroGen
                                                                                                                               Homo sapiens (human)
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HTC; CNSLT_CDNA.
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Submitted (20-UUL-2004) Genoscope - Centre National de Sequencage :
BP 191 9106 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr
Web : www.genoscope.cns.fr)
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                                                                                     TGGAGACTGGCAGTGTCCCAATCCGGGTTGTGGAAACCAGAACTTCGCCTGGAGAACAGA
                                                                                                                                    <u>AAGAGGACCCCGGGGGTTCCCCGAGGGAACCCCTCTGGAGGAGGAAACGTCCAGCACCGAGC</u>
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/mol type="mRNA"
/db_xref="taxon:9606"
/clone="CSODEOOSYF11"
/tissue_type="Placenta"
/plasmid="pCMVSPORT_6"
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                               61
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1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pcMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2236)
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HTC; CNSLT_CDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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                                                                                                                                                      Similarity
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CATGGATGAAGGACCAGATCTTGATCTAGGCCCACCTGTAGATCCAGATGAAGACTCTGA
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                                                                                                    AGGACGCGGTGGAATGGGCAGCGCTGGAGAGCGAGGTGGCTTCAATAAGCCTGGTGGACC
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                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODJO13YN08"
/tissue_type="T_cells (Jurkat cultissue_type="T_cells")
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Pred. No. 6.2e-211;
0; Mismatches 12;
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and Hayashizaki,Y
                                   Chordata; (Rodentia;
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                                 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                       mRNA linear
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oma homolog, full
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E 6 (bases 1 to 1379)

Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, X., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, R., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, Y., Sano, H., Sasaki, D., Saito, H., Saito, R., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
                                               Direct Submission

Submitted (10-UTL-2000) Yoshihide Hayashizaki, The Institute of Submitted (10-UTL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoham RIKEN Yokohama (E-mail:genome-res@gsc.riken.jp, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Pax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y., RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
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Analysis of the mouse transcriptome of 60,770 full-length cDNAs
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                                                                                                                                                                                                                                                                                 Please visit our web site (http://genome.gsc.riken.jp/)
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                                                                                                          GCAGGGGATGCCACCACTTCGTGGAGGTCCTGGTGGCCCAGGAGGCCCTGGAGGAC
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  GAGGCTCCAGAGGAAACCCCTCTGGAGGAGGAAATGTCCAGCACCGAGCTGGAGACTGGC
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/db xref="G1:12852168"
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/tabanelation="Losagergefenkpagpmdegpdldlglp1dpdedsdnsa1yvQg
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LNDNVTLDDLADFFKQCGVVKMNKRTGQPMIHIYLDKETGKPKGDATVSYEDPPTAKA
AVEWFDGKDFQGSKLKVSLARKKPPMNSMCGMPPREGRGMPPLRGGPGGPGGPGGP
MGRWGGRGGJDRGGFPRGSFGNPSGGRNGVHAADDWQCNNFGCNNDFJMRTECN
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/mol type="mRNA"

/strain="C57BL/6J"

/strain="T57BL/6J"

/db_xref="FANTOM DB:3300002D11"

/db_xref="taxon:10090"
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(MGD|MGI:99960, GB|NM_007968, evidence: BLASTN, 99%,
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The RIKEN Genome Exploration FANTOM Consortium.

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                                          sequencing programme residence Res. 20530913
                                                          Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harda, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system—384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence.
AK019460
                                                                                                                                                                                                                                                                                                                                               Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komo, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
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HTC; CAP trapper.
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High-efficiency full-length cDNA
Meth. Enzymol. 303, 19-44 (1999)
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

All Nature 420, 563-573 (2002)

CE 6 (bases 1 to 2107)

RS Adachi J., Alzawa K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayateu, N., Hiramoto, K., Furuno, M., Hanagaki, T., Mara, A., Hayateu, N., Hiramoto, K., Furuno, M., Hanagaki, T., Mara, T., Myazaki, A., Nishi, K., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Myazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Salto, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Salto, H., Saito, H., Sasaki, T., Tanaka, Y., Toya, T., Yamamura, T., Yasunishi, R., Tanaka, T., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Polynor, Suhmisain, M., Muzamatsu, M. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (18-AUG-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:genome-res@gsc.riken.jp, URLihitpi//genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Please visit our web site (http://genome.gsc.riken.jp/) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
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GGGGCCCCTGGACCTTTGATGGAACAGATGGGAGGAAGAAGAGGAGGAGGACGTGGAGGACC CCGTGGTGGCCGGGGCATGGACCGAGGTGGCTTTTGGTGGAGGAAGACGAGGTGGCCCTGG GGACCGTGGTGGTCCTGGAGGAATGTTCAGAGGTGGCAGAGGTGGAGACAGAGGAGGCTT GGATCGTGGTGGTCCCGGTGGAATGTTCAGAGGTGGCCGTGGTGGAGACAGAGGTGGCTT GGGTGGTGATCGTGGCAGAGGTGGCCCTGGTGGCATGCGGGGAAGAAGAGGTGGCCTCAT ATGCAACCAGTGTAAGGCCCCTAAGCCCGAGGGCTTCCTCCCGCCACCCTTTCCACCTCC GTGCAACCAGTGTAAGGCCCCAAAGCCTGAAGGCTTCCTCCCGCCACCCTTTCCGCCCCC TGGAGACTGGCAGTGTCCCAATCCGGGTTGTGGAAACCAGAACTTCGCCTGGAGAACAGA AAGAGGGCCCCGAGGCTCCAGAGGAAACCCCCTCTGGAGGAGGAAATGTCCAGCACCGAGC AAGAGGACCCCGGGGTTCCCGAGGGAACCCCCTCTGGAGGAGGAAACGTCCAGCACCGAGC CCCTGGAGGACCCATGGGTCGCATGGGAGGCCGTGGAGGACAGAGGGGGGCTTCCCTCC ACCCCGTGAGGGCAGAGGCATGCCACCACCCCGTGGAGGTCCAGGAGGCCCAGGAGG ACTTAAAGTCTCCCTTGCTCGGAAGAAGCCTCCAATGAACAGTATGCGGGGTGGTCTGCC TCCACCAACTGCAAAGGCTGCCGTGGAATGGTTTGATGGGAAAGATTTTCAAGGAAGCAA CCCACCCACTGCCAAGGCTGCCGTGGAATGGTTTGATGGGAAAGATTTTTCAAGGGAGCAA TATCTACCTGGATAAGGAGACAGGAAAGCCTAAAGGGGGACGCCACAGTGTCCTATGAAGA CATCTACCTGGACAAGGAAACAGGAAAGCCCCAAAGGCGATGCCACAGTGTCCTATGAAGA CTTCTTTAAGCAGTGTGGGGGTTGTTAAGATGAACAAGAGAGAACTGGGCAACCCCATGATCCA CAACAGTGCAATTTATGTGCAAGGATTAAATGACAATGTGACTCTGGATGATCTGGCAGA CAACAGTGCAATTTATGTACAAGGATTAAATGACAGTGTGACTCTAGATGATCTGGCAGA CATGGATGAAGGACCAGATCTTGATCTAGGCCTTCCTATAGATCCCGATGAAGACTCTGA AGGACGCGGTGGAATGGGCAGCGCTGGAGAGCGAGGTGGCCTTCAATAAGCCTGGTGGACC TGGAGACTGGCAGTGTCCCAATCCGGGCTGTGGAAAACCAGAACTTCGCTTGGAGAACAGA ACTTAAAGTGTCTCTTGCCCGAAAGAAGCCTCCAATGAACAGCATGCGGGGAAGGCATGCC CTTCTTTAAGCAGTGTGGGGTTGTCAAGATGAACAAGAGAACTGGACAACCCATGATCCA CATGGATGAAGGACCAGATCTTGATCTAGGCCCACCTGTAGATCCAGATGAAGACTCTGA 86.9%; 91.7%; 0; Score 879.2; DB 3; Pred. No. 9.4e-208; Mismatches 84; Indels 0; Gaps 480 420 300 120 1869 1809 1749 1689 1629 660 600 540 1389 1329 1269 1149 180 1029 960 900 840 1569 1509 1449 360 1209 240 1089 60 720 0

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                     Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanaggki,T., Hara,A., Hashizume,W., Hayatsu,N., Hiramcto,K., Hiracka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2373)
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HTC; CAP trapper.
  Submitted (16-JUL-2001) Yoshihide Hayashizaki,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The FANTOM Consortium and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FANTOM Consortium.
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19–44 (1999)
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Please visit our web site for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Ri
Genomic Sciences Center and Genome Science Laboratory in RIKEN
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URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
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TCCTGGGGGACCCATGGGTCGCATGGGAGGCCGTGGAGGAGATAGAGGAGGCTTCCCTCC 540
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ilarity 91.5%;
Conservative
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evidence: BLASTN, 99%, match=2172)
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2358. .2363
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/dev_stage="12 days embryo"
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                                                                                                                                                                                                                       Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqrefogenoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1020)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization
Unpublished (2001)

Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BX387336 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens CDNA Clone CSODD004YE17 3-PRIME, mRNA sequence.
BX387336.1 GI:30455516
EX387336.1 GI:30455516
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                                                                                                                                                                      more information about this cluster, see
p://www.genoscope.cns.fr/cdna?s=CS6AD001ZD03NP1&c=10589.f.
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tissue_type="NEUROBLASTOMA COT 50-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT).
                                                            /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODD004YE17"
                                                                                                                                                        Location/Qualifiers
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Pred. No. 9.1e-197;
1; Mismatches 8;
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AK049743.1 GI:26093614
HTC; CAP trapper.
Mus musculus (house mouse
Mus musculus
                                                                                                                                                                                                                                                                            Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashidak, K., Hayatsu, N., Hiramotto, K., Hiramoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nishi, K., Nomura, T., Miyazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takada, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Group Phase I & II Team.

Analysis of the mouse transcriptome based on of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases 1 to 2269)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus 12 days embryo spinal cord cDNA, RIKEN full-length enriched library, clone:C530046A18 product:Ewing sarcoma homolog, full insert sequence.
                                                                                                              Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoha Kanagawa 230-0045, Japan (B-mail:genome-resegsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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Meth. Enzymol. 3
99279253
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Mammalia; Eutheria; Rodentia;
                                                                                             Fax:81-45-503-9216)
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Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/.
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
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evidence: BLASTN, 99%, match=2172)
putative"
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Search completed: February 20, 2005, 16:17:55 · Job time : 2994.19 secs

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SUMMARIES

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ALIGNMENTS

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25-APR-2003; 2003US-0465692P.
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                                                                                                                                                                                                               Homo gapiens
                                                                                                                                                                                                                           human; Ewing sarcoma; EWS; prostatic cancer; alopecia; acne; hypogonadism; androgen-resistance syndrome; testicular feminisation.
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Determining the hormonal effects of substances, used to identify pharmaceuticals, e.g. for treatment of androgen receptor dysfunction, from modulating interaction between nuclear receptors and Ewing sarcoma

N-PSDB; ADS16277. WPI; 2004-627861/61.

Disclosure; SEQ ID NO 2; 30pp; German.

This invention relates to a novel modulators that alter the interaction between the Ewing sarcoma protein (EWS) and its nuclear receptor, as well as the screening method thereof. Specifically, it refers to determining and identifying a hormonal effect brought about by test compounds that modulate either the binding of EWS to the nuclear receptor or the ligand-induced activity of this receptor. The present invention describes the nuclear receptors as including oestrogen, progestorne, thyroid hormone, Vitamin D, and retinoic acid receptors, most preferably they are androgen receptors. Accordingly, these modulators may be used in the development of pharmaceutical compositions that can diagnose and be used to treat

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RESULT 2
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Tumour-associated antigenic target; TAT; human; overexpression; tumour; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; overian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cance cervical cancer; melanoma; leukaemia; hybridisation probe;
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Pred. No. 1.4e-216;
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chromosome identification; chromosome mapping; gene mapping; gene therapy; cytostatic.
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15-APR-2004

29-SEP-2003; 2003WO-US028547.

02-OCT-2002; 2002US-0414971P.

(GETH) GENENTECH INC.

Ξ Ţ, zhang z,

2004-347921/32.

New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or prostate cancer or tumor.

ID NO 5990; 7273pp; English.

The invention relates to human tumour-associated antigenic target (TAT) cc polypeptides, and their related nucleic acids. The TAT polypeptides are coverexpressed in cancer tissues compared to normal tissues, and may thus gerve as effective targets for the diagnosis and treatment of cancer in cc mammals. The invention also relates to nucleic acid and polypeptide ce gequences at least 80% identical to the TAT nucleic acids and compression vectors and host cells comprising a TAT nucleic cold; an antibody specific for a TAT polypeptide; a peptide or organic colorcule which binds to a TAT polypeptide; appetide or organic colorcule which binds to a TAT polypeptide; an acid may thus comprising a compression or cancer in mammals. TAT polypeptides, nucleic acids, cancer in mammals. TAT polypeptides, nucleic acids, contibodies, antagonists, binding molecules and compositions are useful concreased TAT expression, particularly cancers such as breast cancer, colorcetal cancer, lung cancer, ovarian cancer, liver cancer, bladder colorcetal cancer, melanoma and leukaemia. TAT nucleic acids may further be cused as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence cc crepresents a TAT polypeptide of the invention

Sequence 656 AA;

Best Local Sim Matches 656; Query Match Best Local Similarity Conservative 100.0%; 0, Score 3633; Pred. No. 1. Mismatches 1.4e-216; B 8 <u>,</u> Length Indels 0 Gaps 0

5 밁 S 밁 Ś 밁 8 Ś 片 밁 181 121 241 241 181 121 61 19 1 MASTDYSTYSQAAAQQGYSAYTAQPTQGYAQTTQAYGQQSYGTYGQPTDVSYTQAQTTAT NOTAPASAGAGYSSOGOYSSAGAGYSTANGAGYSSYGOGSSYGOGSSYGOGOSSYGOGOSTAGAGY QPAYPAYGQQPAATAPTRPQDGNKPTETSQPQSSTGGYNQPSLGYGQSNYSYPQVPGSYP YGQTAYATSYGQPPTGYTTPTAPQAYSQPVQGYGTGAYDTTTATVTTTQASYAAQSAYGT WASTDYSTYSQAAAQQGYSAYTAQPTQGYAQTTQAYGQQSYGTYGQPTDVSYTQAQTTAT PPQTGSYSQAPSQYSQQSSSYGQQSSFRQDHPSSMGVYGQESGGFSGPGENRSMSGPDNR QPAYPAYGQQPAATAPTRPQDGNKPTETSQPQSSTGGYNQPSLGYGQSNYSYPQVPGSYP PPQTGSYSQAPSQYSQQSSSYGQQSSFRQDHPSSMGVYGQESGGFSGPGENRSMSGPDNR MOPVTAPPSYPPTSYSSTOPTSYDOSSYSOOMTYGOPSSYGOOSSYGOOPPTSY 300 300 240 240 180 180 120 120 60 60

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Thomas
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26-MAY-1994
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The probes 22RR3 and 22RR12 were used to screen a human foetal brain cDNA library (Stratagene cat.# 936206). The clone BF1AC5 was identified and sequenced. It represents the entire coding region and 3'-UTR of the Ews
                                                                                                                                      New nucleic acid of EWS gene and its hybrid(s) - contg. gene sequence involved in chromosomal trans-location, also derived mRNA, probes, fusior proteins etc., for diagnosis and treatment of Ewing sarcoma and melanoma.
                                                                                                                                                                                                                                          WPI; 1993-386580/48.
N-PSDB; AAQ50643.
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655; Conser
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                                                                                                                                                                           factor; Tat-SF1; transcriptional activity factor; HIV-1;
therapy; EWS.
  /note= "imperfect
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Pred. No. 4.9e-216;
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Best Local S
Matches 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EWS is a member of a novel family of putative transcription factors that have RNA recognition motifs and which are frequently associated with many types of sarcomas. It shows homology to a novel human transcriptional activity factor, Tat-stimulatory factor (Tat-SF1, see AAW33811), that is involved in the regulation of transcriptional elongation of HIV-1 by Tat, is essential for Tat trans-activation and is a substrate of an associated cellular kinase. Tat-SF can be used to screen for binding agents useful in the treatment of HIV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid encoding Tat stimulating factor protein and transformed cells - proteins and binding agents, used to immunodeficiency virus infection.
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13-DEC-1996;
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GGPMGRMGGRGGDRGGFPPRGPRGSRGNPSGGGNVQHRAGDWQCPNPGCGNQNFAWRTEC
                                                              PTAKAAVEWFDGKDFQGSKLKVSLARKKPPMNSMRGGLPPREGRGMPPPLRGGPGGPGGP
                                                                                                     SAIYVQGLNDSVTLDDLADFFKQCGVVKMNKRTGQPMIHIYLDKETGKPKGDATVSYEDP
                                                                                                                         SAIYVQGLNDSVTLDDLADFFKQCGVVKMKRTGQPMIHIYLDKETGKPKGDATVSYEDF
                                                                                                                                                              GRGRGGFDRGGMSRGGRGGGRGGMGSAGERGGFNKPGGPMDEGPDLDLGPPVDPDEDSDN
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                                             PTAKAAVEWFDGKDGQGSKLKVSLARKKPPMNSMRGGLPPREGRGMPPPLRGGPGGPGGP
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Pred. No. 3.1e-21
0; Mismatches
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RESULT 5
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AD ABG06460
AX ABG0

                                                                                                                       The invention relates to isolated polynucleotide (I) and polypeptide (II) creation (PCR) primers, oligomers, and for chromosome and gene mapping, comeation (PCR) primers, oligomers, and for chromosome and gene mapping, comed in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed comes. (I) is useful in gene therapy techniques to restore mormal comestivity of (II) or to treat disease states involving (II). (II) is useful in gene therapy techniques to restore mormal complement. (II) and its binding partners are useful in medical imaging complement. (II) and its binding partners are useful in medical imaging complement. (II) and its binding partners are useful in medical imaging complymentials and polynucleotide sequences have applications in collypeptide and polynucleotide sequences have applications in collypeptide and polynucleotide sequences have applications in compositions, foremaics, gene mapping, identification of mutations compositions forematics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and cannot acid sequences of the invention. Note: The sequence data for this composition acid sequences of the invention. Note: The sequence data for this composition in the printed specification, but was obtained in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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23-AUG-2000; 2000US-00649167.
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                                                                                                  patent did not appear in the printed specification, electronic format directly from WIPO at
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Best Local Similarity
Matches 652; Conserv
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                          18-MAY-2000; 2000JP-00145977
                                                      18-MAY-2001;
                                                                                                        WO200188188-A2
                                                                                                                                                              vasospastic
                                                                                                                                                                         Mouse; ischaemia;
                                                                                                                                                                                                 Mouse ischaemic condition related protein sequence SEQ ID NO:289
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                                                                                                                                                            ischaemia; ischaemic
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                                                      2001WO-JP004192
                                                                                                                                                                                                                              (first
                                                                                                                                                                       compressive ischaemia; occlusive ischaemia;
                                                                                                                                                                                                                                                                                  protein;
                                                                                                                                                                                                                             entry)
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99.2%;
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Pred. No. 1.4e-214;
1; Mismatches 3;
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                                                                                                                                                            condition; ischaemic disease
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Ishikawa K,
                                              2002-034733/04
                                             ABI99383.
                                                  Asai S,
                                                  Takahashi
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                                                  Nagata
                                                  'n
                                                  Ishii
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Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these

Claim 2; Page 799-802; 2690pp; English.

The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (1) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (1). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (AB199202 to AB19912, encoding the protein sequences in ABB57020 to ABB57374) or by determining the expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition-improving drugs or therapeutics for ischaemic diseases. AB199913 and AB199914 represent PCR primers for a mouse ischaemic condition related sequence, which are used in the condition is the condition are used in the condition are used to the condition related sequence, which are used in the condition related sequence, which are used the condition related sequence, which are used to the condition related sequence, which are used the condition related sequence. in the exemplification of the present invention

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                   NQCKAPKPEGFLPPPFPPPGGDRGRGGGPGGMRGGRGGLMDRGGPGGMFRGGRGGDRGGFR
                                                                             GGPMGRMGGRGGDRGGFPPRGPRGSRGNPSGGGNVQHRAGDWQCPNPGCGNQNFAWRTEC
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                                                           GGPMGRMGGRGGDRGGFPPRGPRGSRGNPSGGGNVQHRAGDWQCPNPGCGNQNFAWRTEC
                                                                                                                                        PTAKAAVEWFDGKDFQGSKLKVSLARKKPPMNSMRGGLPPREGRGMPPPLRGGPGGPGGP
                                                                                                                                                                                  SAIYVQGLNDNVTLDDLADFFKQCGVVKMNKRTGQPMIHIYLDKETGKPKGDATVSYEDP
                                                                                                                                                                                                 SAIYVQGLNDSVTLDDLADFFKQCGVVKANKRTGQPMIHIYLDKETGKPKGDATVSYEDP
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NQCKAPKPEGFLPPPFPPPGGDRGRGGPGGMRGGRGGLMDRGGPGGMFRGGRGGDRGGFR
                                                                                                                     PTAKAAVEWFDGKDFQGSKLKVSLARKKPPMNSMRGGMPPREGRGMPPPLRGGPGGPGGP
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Pred. No. 8.7e-213;
B; Mismatches 4;
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(UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.

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RESULT 7
ADAS5145
AC ADAS
XX ADAS
XX ADAS
XX Cytc
DT 20-N
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Best Local S
Matches 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to novel human secretory or membrane proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-ADA54071). The coding sequences are useful in the gene therapy of diseases caused by abnormalities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 14; SEQ ID NO 2713; 205pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polynucleotides encoding full-length polypeptides, e.g. secretory and/or membrane proteins, useful for developing medicines for diseases which the gene is involved, or as target molecules for gene therapy.
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24-JAN-2002; 2002US-0350435P.
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DB; ADA53506.
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RES ASSOC BIOTECHNOLOGY.
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                                                                                                           QPAYPAYGQQPAATAPTRPQDGNKPTETSQPQSSTGGYNQPSLGYGQSNYSYPQVPGSYP
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MQPVTAPPSYSPGTSYSSTQFTSYDGSYSQQNTYQQPSSYGQQSSYGQQSYGQQPTYSY
                                                                                                                                                                               YGQTAYATSYGQPPTGYTTPTAPQAYSQPVQGYGTGAYDTTTATVTTTQASYAAQSAYGT
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                                                                           QPAYPAYGQQPAATA----
                                                                                                                                                                                                            YGQTAYATSYGQPPTGYTTPTAPQAYSQPVQGYGTGAYDTTTATVTTTQASYAAQSAYGT
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ilarity 91.3%;
Conservative
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Hio Y, Otsuka K, Nagai K,
Otsuka M, Nagahari K, Mas
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Pred. No. 1.3e
0; Mismatches
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1.3e-194;
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Masuho Y;
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This invention

relates

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isolated full length

human

CDNA

Claim 1;

SEQ ID NO 2908;

2686pp; novel,

English.

New 1995 cDNA, useful Alzheimer's diseases,

for treating osteoporosis, neurological diseases, Parkinson's diseases, dementia and various cancer

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RESULT 8
ADRO9402
ID ADRO
XX ADRO
AC ADRO
DT 04-N
XX Huma
XX Huma
XX Huma
XX Sens
XX Sens
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XX Sens
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                                                                                                                                                                                                                                                                                                                                                                                  14-FEB-2003; 2003JP-00102207.
09-MAY-2003; 2003JP-00131452.
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                                                                                                                                                                                                                                                         Wakamatsu
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CC molecules and the encoded proteins thereof. Specifically, it refers to CC cDNA clones obtained by an oligo-capping method, where none of these CC clones are identical to any known human mRNAs. The present invention; ... CC describes an immunoassay to identify agonists and antagonists, as well as CC antibodies, antisense molecules and siRNAs that can all be used to bind CC to and modulate expression of the cDNA molecules. As such, these CC molecules are useful for diagnostic markers or therapeutic targets for CC the various diseases or morbid states. In particular, they are useful in CC gene therapy for treating osteoporosis, neurological disease, Alzheimer's CC disease, Parkinson's disease, dementia, short memory and various cancers, CC as well as for maintaining equilibrium of sense or motor function, and CC for treating emotional reaction, fear response and panic. Accordingly, CC they exhibit osteopathic, neuroprotective, noutropic, antiparkinsonian, CC cytostatic and tranquiliser activities. This polypeptide is a protein CC encoded by a full length human cDNA sequence of the invention. NOTE: This sequence is not given in the sequence listing of the specification but CC can be obtained on CD-ROM from the European Patent Office, Vienna Sub-
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604 ₽,

Query Match

Length 604;

밁 र्ठ 밁 S 밁 S 밁 Ş 밁 र् 밁 र् 문 δ 문 S 밁 S 밁 Ś 489 429 481 369 421 309 361 301 249 189 241 154 181 100 -----YSQQPAATAPTRPQDGNKPTETSQPQSSTGGYNQPSLGYGQSNYSYPQVPGSYP 121 590; 13 1 MASTDYSTYSQAAAQQGYSAYTAQPTQGYQATQAYGQQSYGTYGQPTDVSYTQAQTTAT Similarity SA I YVQGLNDSVTLDDLAD FFKQCGVVKMNKRTGQPMIHIYLDKETGKFKGDATVSYEDF QPAYPAYGQQPAATAPTRPQDGNKPTETSQPQSSTGGYNQPSLGYGQSNYSYPQVPGSYP GGRGMDRGGFGGGRRGGPGGPGGPMGGRRGGRGGPGKMDKGEHRQERRDRPY PTAKAAVEWFDGKDFQGSKLKVSLARKKPPMNSMRGGLPPREGRGMPPPLRGGPGGPGGP GRGRGGFDRGGMSRGGRGGGGGGGGSAGERGGFNKPGGPMDEGPDLDLGPPVDPDEDSDN PPQTGSYSQAPSQYSQQSSSYGQQSSFRQDHPSSMGVYGQESGGFSGPGENRSMSGPDNR GGRGMDRGGFGGGRRGGPGGPPGPLMEQMGGRRGGRGGPGKMDKGEHRQERRDRPY NOCKAPKPEGFLPPPFPPPGGDRGRGGPGGMRGGRGGLMDRGGPGGMFRGGRGGDRGGFR NQCKAPKPEGFLPPPFPPPGGDRGRGGPGGMRGGRGGIMDRGGPGGMFRGGRGGDRGGFR GGPMGRMGGRGGDRGGFPPRGPRGSRGNPSGGGNVQHRAGDLQCPNPGCGNQNFAWRTEC GGPMGRMGGRGGDRGGFPPRGPRGSRGNPSGGGNVQHRAGDWQCPNPGCGNQNFAWRTEC PTAKAAVEWFDGKDFQGSKLKVSLARKKPPMNSMRGGLPPREGRGMPPPLRGGPGGPGGP SATYVQGLNDSVTLDDLADFFKQCGVVKMNKRTGQPMIHIYLDKETGKPKGDATVSYEDP GRGRGGFDRGGMSRGGRGGGRGGMGSAGERGGFNKPGGPMDEGPDLDLGPPVDPDEDSDN PPQTGSYSQAPSQYSQQSSSYGQQSSFRQDHPSSMGVYGQESGGFSGPGENRSMSGPDNR YGOTAYATSYGOPPTGYTTPSYPPT-----SYSSTQPT-----SYDQSS----YGQTAYATSYGQPPTGYTTPTAPQAYSQPVQGYGTGAYDTTTATVTTTQASYAAQSAYGT 120 88.4%; nilarity 89.9%; Conservative Score 3210; DB 8; Pred. No. 1.9e-190; 3; Mismatches 11; -----SYGQQSSYGQQSSYGQQPPTSY Indels 52; Gaps 656 604 548 600 488 540 480 420 308 360 248 300 188 153 180 99 60 428 368

The present invention describes an isolated PRO nucleic acid (I). Also CC described: (I) a vector comprising (I); (2) a host cell comprising the CC vector of (I); (3) a process for producing a PRO polypeptides; (4) an CC isolated PRO polypeptide; (5) a chimeric molecule comprising the CC polypeptide of (4) fused to a heterologous amino acid sequence; (6) an CC antibody which specifically binds to a polypeptide of (4); (7) a CC composition of matter comprising a polypeptide of (4), an agonist or CC polypeptide in combination with a carrier; (8) an article of manufacture comprising a container, a label on the container and a composition of CC matter of (7); (9) a method of treating an immune related disease in a CC mammal; (10) a method for determining the presence of a PRO polypeptide CC in a sample suspected of having the polypeptide; (11) a method of identifying a compound that inhibits or CC mimics the activity of or expression of a gene encoding a PRO polypeptide CC antiatsthmatic, antidlabetic, antiinflammatory, antiarchitic, CC antiatsthmatic, antidlabetic, antiantallari, antiantallari, compound that inhibits or CC insphrotropic, neuroprotective, osteopathic, respiratory, vasorropic and CC virucide activity end can be used in gene therapy. The nucleic acid CC virucide activities, and can be used in gene therapy. The nucleic acid CC virucide activities, and can be used in gene therapy. The nucleic acid CC virucide activities, and can be used in gene therapy. The nucleic acid CC virucide activities, and can be used in gene therapy. The nucleic acid CC virucide activities, and can be used in gene therapy. The nucleic acid CC virucide activities or compositions, kits and methods are CC virucide of the polypeptides. The present sequence represents a human CCC protein from the present invention. Aggarwal S, C human; PRO; immune related disease; inflammatory immune response; immune response stimulation; antiallergic; antianaemic; antiarthritic; antialsthmatic; antidiabetic; antiinflammatory; antipsoriatic; antitheumatic; antithyroid; CNS; dermatological; gastrointestinal; haemostatic; hepatotropic; immunostimulant; immunosuppressive; muscula: nephrotopic; neuroprotective; osteopathic; respiratory; vasotropic; immunostimulant; respiratory; vasotropic; respiratory; respiratory; vasotropic; respiratory; vasotropic; respiratory; respi New PRO polynucleotides and polypeptides, useful in useful in diagnosing and treating an immune related disease, e.g. systemic lupus erythematosus, rheumatoid arthritis, diabetes mellitus or asthma and in Claim 1; SEQ ID NO 2310; 3009pp; English erythematosus, rheumatoid arthr stimulating an immune response. 29-OCT-2002; 2002US-0422472P 28-OCT-2003; 2003WO-US034381. 13-MAY-2004 WO2004039956-A2 virucide; 18-NOV-2004 Homo sapiens (GETH) GENENTECH INC 2004-376182/35. DB; ADP56333. PRO protein sequence gene therapy. Clark H, (first entry) Gurney SEQ ID NO:2310 Æ, Schoenfeld immunosuppressive; muscular; ۲

Sequence 583 ₹

RESULT 9 ADP56334 ID ADP5

ADP56334 standard;

protein; 583

-Matches 582; Query Match Best Local Similarity Conservative 87.5%; 0; Score 3178.5; Pred. No. 1.6 Mismatches .6e-188; DB 8; Indels 583; 73; Gaps 1;

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RESULT 10
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     02-OCT-2002; 2002US-0414971P
                                                                                                                                                                          WO2004030615-A2
                                                       29-SEP-2003; 2003WO-US028547;
                                                                                                                  15-APR-2004.
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Sequence 361 AA;

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The invention relates to human tumour-associated antigenic target (TAT) CC polypeptides, and their related nucleic acids. The TAT polypeptides are coverexpressed in cancer tissues compared to normal tissues, and may thus CC serve as effective targets for the diagnosis and treatment of cancer in C mammals. The invention also relates to nucleic acid and polypeptide sequences at least 80% identical to the TAT nucleic acids and codypeptide; expression vectors and host cells comprising a TAT nucleic acid; an antibody specific for a TAT polypeptide; fusion proteins comprising a CC molecule which binds to a TAT polypeptide; fusion proteins comprising a CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids and CC antibodies, antagonists, binding molecules and compositions are useful CC increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder CC cancer, pancreatic cancer, cervical cancer, cancers of the central CC cancer, pancreatic cancer, cervical cancer, cancers of the central CC cancer, pancreatic cancer, cervical cancer, cancers of the central CC cancer, pancreatic cancer, cervical cancer, cancers of the central CC cancer, pancreatic cancer, cervical cancer, cancers of the central CC cancer, pancreatic cancer, cervical cancer, cancers of the central CC cancer as hybridisation probes, in chromosome and gene mapping, in CC chromosome identification and in gene therapy. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 12; SEQ ID NO 491; 7273pp; English
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343

ALGGERTFOUTNGRKKER

360

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CC The invention describes a method of treating genetically-defined disease CC associated with chromosomal abscrations yielding oncogenic fusion proteins (I), treating cancerous cells containing (I) in a heterogeneous cell population, treating proliferative diseases associated with mutant protein or cellular protein isoforms (II) dependent on heat shock protein (HSP)-90, or selectively treating cells expressing (II) involving CC daministering HSP90-inhibitor. The method is useful for treating concogenic fusion protein, treating centerous cells containing fusion or concogenic fusion protein, treating cancerous cells containing fusion or concogenic fusion protein, treating cancerous cells containing fusion or cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g. rheumatoid arthritis or cancer) associated with mutant protein or cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g. CC protein isoform in a patient heterozygous for (II). The method is useful for treating a disease e.g. haematopoictic disorder such as T or B cell (T protein soform a disease e.g. haematopoictic disorder such as T or B cell (T protein) are characterised by a solid tumour such as papillary thyroid corrections. Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and corrections. This represents a protein encoded by the DNA sequence of a chromosome aberration
                                                                                                                                                  Query Match
Best Local S
Matches 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 204-206; 389pp; English.
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MASTDYSTYSQAAAQQGYSAYTAQPTQGYAQTTQAYGQQSYGTYGQPTDVSYTQAQTTAT
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                                                                                                                                              Score 1429; DB 5;
Pred. No. 2.6e-80;
6; Mismatches 16
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             The present sequence represents a chimeric human Ewing's sarcoma (EWS)-WT1 protein. EWS is also known as peripheral neuroectodermal tumour (PNET). The protein is composed of EWS and WT1 proteins (see features table). The WT1 gene encodes 4 alternatively spliced RNA transcripts that produce functionally different products. One alternative splice site is at the 3' end of exon 9 and leads to products that differ by 3 amino acids placed between the third and fourth zinc fingers of the DNA binding domain. The present protein does not contain these three amino acids (Lys, Thr, Ser), while AAM34971 does. Detection of EWS-WT1 can be accomplished by reverse transcriptage PCR, where WT1 is screened (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ewing's sarcoma; EWS; EWS-WT1 protein; peripheral neuroectodermal tumour; PNET; breakpoint locus; Wilms' tumour; desmoplastic small round cell tumour; DSRC tumour.
                                                                                                                                                                        Disclosure; Col 39-42; 34pp; English
                                                                                                                                                                                                                   Diagnosis of desmoplastic small round cell tumours -
                                                                                                                                                                                                                                                                                        Ladanyi M, Gerald W;
                                                                                                                                                                                                                                                                                                                                                                            08-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric Ewing's sarcoma-WT1 protein splice variant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein
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                                                                                                                                                                                                   encoding chimeric
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "EWS protein"
265. .362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "WT1 protein'
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RESULT 13
AAW34971
ID AAW34
XX AAW34
XX AAW34
XX O9-MA
XX Ewing
KW Ewing
KW PNET;
KW desmo
OS Homo
OX Homo
OX Homo
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oligonucleotides based on the AAT97869 are used in a method for the diagnosis of DSRC tumours in patients. The method comprises detecting a nucleic acid molecule encoding a chimeric EWS-WT1 protein in a sample from the subject, where positive detection indicates the presence of a DSRC tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tumour, which shares some histopathologic features of desmoplastic small round cell (DSRC) tumours. The EWS-WT1 chimeric transcript has been detected in 11 out of 12 DSRC tumours studied and in none of 49 other tumours. DSRC tumours are associated with translocation of the EWS gene.
  N-PSDB; AAT97869.
                          WPI; 1997-479448/44
                                                                                                                                                                                 08-MAY-1995;
                                                                                                                                                                                                                                 08-MAY-1995;
                                                                                                                                                                                                                                                                                   23-SEP-1997.
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                                                                          Ladanyi M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                            Gerald W;
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                                                                                                                                                                                                                                 95US-00437027
                                                                                                                                                                                                                                                                                                                                                                                                                /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sarcoma-WT1 protein splice variant 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            round cell tumour;
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Pred. No. 6.9e-80;
0; Mismatches 0;
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Diagnosis of desmoplastic small round cell tumours - acid encoding chimeric EWS-WT1 protein. by detecting nucleic

Disclosure; Col 37-40; 34pp; English

The present sequence represents a chimeric human Ewing's sarcoma (EWS)-CC (WTI) protein. EWS is also known as peripheral neuroectodermal tumour (CC (PNET)). The protein is composed of EWS and WTI proteins (see features table). The WTI gene encodes 4 alternatively spliced RNA transcripts that produce functionally different products. One alternative splice site is at the 3' end of exon 9 and leads to products that differ by 3 amino caids placed between the third and fourth zinc fingers of the DNA binding domain. The present protein contains these three amino acids (Lys, Thr, Ser), while AAW34972 does not. Detection of EWS-WTI can be accomplished by reverse transcriptase PCR, where WTI is screened (see AAT97852-68) as a breakpoint locus because of its involvement in Wilms' tumour, which shares some histopathologic features of desmoplastic small round cell (DSRC) tumours. The EWS-WTI chimeric transcript has been detected in 11 out of 12 DSRC tumours studied and in none of 49 other tumours. DSRC tumours are associated with translocation of the EWS gene.

CO disjonucleotides based on the AAT97869 are used in a method for the CO diagnosis of DSRC tumours in patients. The method comprises detecting a nucleic acid molecule encoding a chimeric EWS-WTI protein in a sample from the subject, where positive detection indicates the presence of a from the subject, where positive detection indicates the presence of a

XFFX#X55555555555555555555555555

Sequence 365 AA;

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Best Local Similarity
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241
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                                                                                                                                                                                                                                         1 MASTDYSTYSQAAAQQGYSAYTAQPTQGYAQTTQAYGQQSYGTYGQPTDVSYTQAQTTAT
               PPQTGSYSQAPSQYSQQSSSYGQQS
                                                  MOPVTAPPSYPPTSYSSTOPTSYDQSSYSQQNTYGQPSSYGQQSSYGQQPPTSY
                                                                   MQPVTAPPSYPPTSYSSTQPTSYDQSSYSQQNTYGQPSSYGQQSSYGQQSSYGQQPPTSY
                                                                                                       QPAYPAYGQQPAATAPTRPQDGNKPTETSQPQSSTGGYNQPSLGYGQSNYSYPQVPGSYP
                                                                                                                        QPAYPAYGQQPAATAPTRPQDGNKPTETSQPQSSTGGYNQPSLGYGQSNYSYPQVPGSYP
                                                                                                                                                        YGQTAYATSYGQPPTGYTTPTAPQAYSQPVGGYGTGAYDTTTATVTTTQASYAAQSAYGT
                                                                                                                                                                                                               MASTDYSTYSQAAAQQGYSAYTAQPTQGYAQTTQAYGQQSYGTYGQPTDVSYTQAQTTAT
PPQTGSYSQAPSQYSQQSSSYGQQS
                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                               39.1%;
100.0%;
                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                               Score 1420; DB 2;
Pred. No. 6.9e-80;
                                                                                                                                                                                                                                                                   Mismatches
265
                       265
                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                          Length 365;
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ADI26113 standard; protein; 518 8

ADI26113

22-APR-2004

(first

entry)

Human protein that promotes STAT6 activation

#39.

RESULT 14
ADI26113
ID ADI26
AC ADI26
AC ADI26
AC ADI26
XX Human
XX human
KW immun
KW immunogen, STATG activation, allergy, inflammation, autoimmune disease diabetes, hyperilpidaemia, infection, cancer, Th1 hyperactive disease, rheumatoid arthritis, osteoarthritis, systemic lugus crythematosus, sepsis, asthma, allergic rhinitis, ischaemic heart disease; subarachnoid human; signal transducer and activator of transcription 6; STAT6; haemorrhage; viral hepatitis; AIDS. disease;

sapiens

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a purified protein promoting signal transducer CC and activator of transcription 6 activation (STAT6). The protein is cuseful for the producing an antibody, which involves administering the CC useful for the spitope-bearing fragments to a non-human animal as an activation. The nucleic acid is useful for diagnosing a disease or CC antigen. The nucleic acid is useful for diagnosing a disease or CC antigen. A transformant expressing the protein is useful for screening CC compounds which inhibit or promote STAT6 activation. A transformant CC expressing the protein is useful for producing a pharmaceutical CC composition. Compositions, antibodies and antisense molecules are useful CC for the treating a disease associated with STAT6 activation such as allergic diseases, inflammation, autoimune diseases, diabetes, CC hyperlipidaemia, infections disease and cancers. Compositions are useful CC for treating disease associated with STAT6 activation and/or prevention CC arthritis, osteoarthritis, systemic lupus erythematosus, sepsis, asthma, CC allergic rhinitis, ischaemic heart diseases, subarachnoid haemorrhage, crimal hepatitis and AIDS. The protein has efficient promoting STAT6 cativation or inhibition of STAT6. The present sequence represents the activation or inhibition of STAT6. The present sequence represents the cc acid acid sequence of a human protein which promotes STAT6 activation.
                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 301; Conserv
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06-JUN-2002; 2002US-0385912P.
26-DEC-2002; 2002JP-00377326.
27-DEC-2002; 2002US-0436467P.
15-MAY-2003; 2003JP-00137505.
16-MAY-2003; 2003US-0470836P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New signal transducer and activator of transcription 6 activation promoting purified protein, for diagnosing and treating disease associated with activation/inhibition of transcription factor e.g. diabetes and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 78; 1368pp;
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DB; ADI26112:
235 QPPTSYPPQTGSYSQAPSQYSQQSSSYGQQSSFRQDHPSSMGVYGQESGGFSGPGENRSM 294
                                                                                                                                                       118 YGTQPAYPAYGQQPAATAPTRPQDGNKPTETSQPQSSTGGYNQPSLGYGQSNYSYPQVPG
                                                                                                                                                                                                                        60 TYGQTAYATSYGQPP-TGYTTPTAPQAYSQPVQGYG-TGAYDTTTATVTTTQASYAAQSA 117
                                                                                                                                                                                              49 GYGQSSYGSSYGQTQNTGYGTQSAP-----
                                                                                                                                                                                                                                                                                                              1 MASTDYSTYSQAAAQQGYSAYTAQFTQGYA-QTTQAYGQQSYGTYGQPTDVSYTQAQTTA 59
                                                                         SYPMQPVTAPPSYPPTSYSSTQPTSYDQSYSSQQNTYGQPSS--YGQQSSY-GQQSSYGQ
                                                                                                                                                                                                                                                                         MASNDYT----QQATQSYGAYPTQPGQGYSQQSSQPYGQQSYSGYGQSAD-----TS
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                                                                                                                                                                                                                                                                                                                                                       35.5%; Score 1290; DB 8;
43.9%; Pred. No. 1.1e-71;
tive 59; Mismatches 128;
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                                                                                                                    ----PSSTSGSYG--
                                                                                                                                                                                              -QGYGSTGGYG-----SSQSSQSS
                                                                                                                                                                                                                                                                                                                                                       128; Indels 198;
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N-PSDB; AAK51488

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RESULT 15
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15-SEP-2000;
20-OCT-2000;
30-NOV-2000;
                                                                                                                                                                                                                                                                                                                                         03-FEB-2000; 2000US-00496914
27-APR-2000; 2000US-00560875
20-UUN-2000; 2000US-00598075
19-UUL-2000; 2000US-00620325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-FEB-2001; 2001WO-US004098
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                                                                                                                                                                                               (HYSE-) HYSEQ INC.
                                                                                             YT, Liu C, Drmanac I
, Zhao QA, Wang D, V
AJ, Yang Y, Wejhrman
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 295 SGPDNRGRGRGGF-----DRGGMSRG------GRGGGRGGMGSAG--ERGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RRGGRGGPGKMD-KGEHRQERRDRPY 656
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; 2000US-00663561.
; 2000US-00693325.
; 2000US-00728422.
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                                                                                     Drmanac RT, ...
ng D, Wang J
                                                                                                  Asundi V, Zh
g J, Zhang J,
Goodrich R;
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J, Ren
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Chen
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Wang
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Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy.
   Claim
20; Page 3253-3254; 6221pp; English.
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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM73823-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor|activity, haematopolesis regulating activity, tissue growth factor activity, inmunomodulatory activity and activity/inhibin activity and 'may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system discorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication

Sequence 526 AA;

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Best Local Similarity
Matches 301; Conserv
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                                                                                                                                                                                                                                                                                 414 TVSYEDPPTAKAAVEWFDGKDFQGSKLKVSLARKKFPMNSMRGGLPPREGRGMPPPLRGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            238 TSYPPQTGSYSQAPSQYSQQSSSYGQQSSFRQDHPSSMGVYGQBSGGFSGPGENRSMSGP 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129 SYSQQP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 178 SYPMQPVTAPPSYPPTSYSSTQPTSYDQSSYSQQNTYGQPSSYGQQSSYGQQSSYGQQPP 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 YGTQPAYPAYGQQPAATAPTRPQDGNKPTETSQPQSSTGGYNQPSLGYGQSNYSYPQVPG 177
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   RQERRDRPY 656
                                                                          -GRGGDRGGFRGGR-GMDRGGFGGGRRGGPGGPPGPLMEQMGGRRGGRGGPGKMD-KGEH 647
                                                                                                            FSWRNECNOCKAPKPDG-----PG-----GGPGGSHMGGNYGDDRRGGRGGYDRGGY
                                                                                                                                              FAWRTECNOCKAPKPEGFLPPPPPPPPGGDRGRGGPGGMR-GGRGGLMDRGGPGGMFRG--
                                                                                                                                                                                                          PGGPGGPGGPMGRMGGRGGDRGGFPPRGPRGSRGNPSGGGNVQHRAGDWQCPNPGCGNQN
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nilarity 45.0%;
Conservative 5
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|Pred. No. 3.6e-71;
59; Mismatches 153;
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                                       GPGKMDSRGEH
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RQDRRERPY 526

Search completed: February 18, 2005, 15:09:03 Job time : 175 secs

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*

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US-09-949-016-10914
US-09-949-016-10915
US-08-437-027-21
US-08-437-027-21
US-08-438-092-1080
US-09-949-016-7825
US-09-931-039-324
US-09-919-039-324
US-08-963-825-21
US-09-919-039-324
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US-09-910-928B-7
US-09-910-928-80-9
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Sequence 2, Appli
Sequence 4, Appli
Sequence 1250, Ap
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Sequence 10915, A
Sequence 21, Appl
Sequence 7825, Ap
Sequence 1080, Ap
Sequence 1080, Ap
Sequence 20, Appl
Sequence 21, Appl
Sequence 22, Appl
Sequence 23, Appl
Sequence 24, Appl
Sequence 25, Appl
Sequence 27, Appl
Sequence 37, Appl
Sequence 39, Appl
Sequence 30, Appl
Sequence 20, Appl
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ALIGNMENTS

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RESULT 1 US-08-343-443B-2 (Sequence 2, Application US/08343443B Patent No. 5968734 Patent No. 5968734 Patent No. 1968734 APPLICANT: Delattre, Olivier APPLICANT: Delattre, Olivier APPLICANT: Delattre, Olivier APPLICANT: Desmaze, Chantal APPLICANT: Decter, Martine APPLICANT: Peter, Martine APPLICANT: Ploougastel, Beatrice APPLICANT: Thomas, Gilles APPLICANT: Thomas, Gilles APPLICANT: CHROMOSOME 22 INVOLVED IN RECURRENT CHROMOSOMAL TITLE OF INVENTION: TRANSLATIONS ASSOCIATED WITH THE DEVELOPMENT OF CANCEROUS TITLE OF INVENTION: TRANSLATIONS ASSOCIATED WITH THE DEVELOPMENT OF CANCEROUS TITLE OF INVENTION: TRANSLATIONS ASSOCIATED WITH THE DEVELOPMENT OF CANCEROUS TITLE OF INVENTION: TRANSLATIONS ASSOCIATED WITH THE DEVELOPMENT OF CANCEROUS TITLE OF INVENTION: TRANSLACATIONS NUMBER OF SEQUENCES: 129 CORRESPONDENCE ADDRESS: ADDRESSEE: Weiser & Associates STREET: 230 South Fifteenth Street CITY: Philadelphia TATE: PA COUNTRY: USA ZIP: 19102

Length

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Gaps

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GENERAL INFORMATION:

APPLICANT: Sharp, Phillip A.

APPLICANT: Sharp, Phillip A.

APPLICANT: Sharp, Phillip A.

APPLICANT: Tand, Order Standard Control of Title OF INVENTION: TAT-SF: Cofactor For Stimulation Of TITLE OF INVENTION: Elongation By HIV-1 TAT FILE OF INVENTION: Elongation By HIV-1 TAT FILE OF INVENTION INDEER: US/09/214,564A

CURRENT APPLICATION NUMBER: US 60/021,218

PRIOR APPLICATION NUMBER: US 60/021,218

PRIOR APPLICATION NUMBER: US 60/033,152

PRIOR APPLICATION NUMBER: US 60/033,152

PRIOR APPLICATION NUMBER: PCT/US97/11713

PRIOR FILING DATE: 1996-07-03

PRIOR FILING DATE: 1997-07-03
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                                                ; Sequence 1250, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
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Best Local Similarity 100.0%;
Matches 656; Conservative 0.
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SOFTWARE: FASTSEQ for
SEQ ID NO 4
LENGTH: 656
 PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
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%; Pred. No. 8.46
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Sequence 10914, Application US/09949016

Patent NO. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF

PILE REPERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20
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US-09-949-016-10914
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; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number Q01844
US-09-538-092-1250
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Best Local Similarity
Matches 656; Conserv
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SEQ ID NO 1250
LENGTH: 656
TYPE: PRT
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 Sequence 10915, Application US/09949016

Sequence 10915, Application US/09949016

Patent No. 6812339

PATENT INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION OF FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755
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PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 10014
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Pred. No. 1.7e-211;
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PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-37,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.
SEQ ID NO 10915
PENCIFE: 591
                                                                                                                                                                         RESULT 6
US-08-437-027-21
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US-09-949-016-10915
                                                                                                                                  Sequence 21, Application US/08437027 Patent No. 5670317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 87.5%;
Best Local Similarity 88.7%;
Matches 582; Conservative
              GENERAL INFORMATION:
APPLICANT: Landany, Marc
APPLICANT: Gerald, William
TITLE OF INVENTION: A DIAGNOSTIC TEST FOR TEST
TITLE OF INVENTION: SMALL ROUND CELL TUMOR
NUMBER OF SEQUENCES: 21
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CORRESPONDENCE ADDRESS:
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Pred. No. 1.7e-211;
0; Mismatches 1;
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US-08-437-027-20
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NAME: White, John P
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 4641
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-298-0400
TELEPHAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 362 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                  Sequence 20, Application US/08437027
Patent No. 5670317
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Landanyi, Marc
APPLICANT: Gerald, William
APPLICANT: Gerald, William
TITLE OF INVENTION: A DIAGNOSTIC TEST FOR THE DESMOPLASTIC
TITLE OF INVENTION: SWALL ROUND CELL TUMOR
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 265; Conserv
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
OPTRATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/437,027
                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
STREET: 1185 Ave.
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
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STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                 ADDRESSEE:
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                                                                                                                                                            E: Cooper & Dunham LLP
1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39.1%; Score 1420; DB 1; ilarity 100.0%; Pred. No. 2.2e-90; Conservative 0; Mismatches 0;
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COMPUTER READABLE FORM:

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US-09-449-016-7825

Sequence 78.5, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THER

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

PRIOR PILING DATE: 2000-09-08

PRIOR PILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08
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TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-437-027-20
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FRANSEQ for Windows Version 4.0
SEQ ID NO 7825
LENGTH: 306
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Best Local Similarity
Matches 265; Conserv
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INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 4641
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212,278-0400
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MASTDYSTYSQAAAQQGYSAYTAQPTQGYAQTTQAYGQQSYGTYGQPTDVSYTQAQTTAT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QPAYPAYGQQPAATAPTRPQDGNKPTETSQPQSSTGGYNQPSLGYGQSNYSYPQVPGSYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPQTGSYSQAPSQYSQQSSSYGQQS 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOPVTAPPSYPPTSYSSTOPTSYDQSSYSQQNTYGQPSSYGQQSSYGQQSSYGQQPPTSY
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; PEATURE;
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P35637
US-09-538-092-1080
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Patent No. 6753314
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuraPatSeqFormatter Version 0.9
SEQ ID NO 1080
LENGTH: 526
                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Giot, Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method
FILE REFERENCE: 15966-542
                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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                                   118 YGTQPAYPAYGQQPAATAPTRPQDGNKPTETSQPQSSTGGYNQPSLGYGQSNYSYPQVPG 177
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                                                                                                                                                                                                                             301; Conservative
                                                                       49 GYGQSSY-SSYGQSQNTGYGTQSTP-----QGYGSTGGYG-----SSQSSQSSQSS 90
                                                                                                           60 TYGQTAYATSYGQPP-TGYTTPTAPQAYSQPVQGYG-TGAYDTTTATVTTTQASYAAQSA 117
                                                                                                                                                                     1 MASTDYSTYSQAAAQQGYSAYTAQPTQGYA-QTTQAYGQQSYGTYGQPTDVSYTQAQTTA
                                                                                                                                                   1 MASNDYT----QQATQSYGAYPTQPGQGYSQQSSQPYGQQSYSGYSQSTD-----TS
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                                                                                                                                                                                                                                             35.3%; Score 1282; DB 4;
45.0%; Pred. No. 1.1e-80;
                                                                                                                                                                                                                             59; Mismatches 153;
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                                                                                                                                                                                                                                                                 DB 4;
-PSSTSGSYGSSS----QSSSYGQPQ-SG
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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 107, Application US/08343443B Patent No. 5968734 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
          COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: AEDIT 1.0 DOS text editor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/343,443B
FILING DATE: 18-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                           STREET: 230 L. CITY: Philadelphia
                                                                                                                                                               COUNTRY:
CLASSIFICATION:
                                                                                                                                                                                                                             ADDRESSEE:
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                                                                                                                                                                                                            2: Weiser & Associates
230 South Fifteenth Street
                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                              Ploougastel, Beatrice
Thomas, Gilles
                                                                                                                                                                                                                                                                                                                                                                                                              Peter, Martine
                                                                                                                                                                                                                                                                                                                                                                                                                              Melot,
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Desmaze, Chantal
                                                                                                                                                                                                                                                                                                                                                              Zucman, Jessica
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                                                                                                             Floppy disk
                                                                                                                                                                                                                                                                                           CHROMOSOME 22 INVOLVED IN RECURRENT CHROMOSOMAL TRANSLATIONS ASSOCIATED WITH THE DEVELOPMENT OF CANCEROUS TUMORS, AND NUCLEIC ACIDS OF FUSION RESULTING FROM SAID
                                                                                                                                                                                                                                                              TRANSLOCATIONS
129
                                                                                                                                                                                                                                                                                                                                               NUCLEIC ACID CORRESPONDING TO A GENE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -PG----GGPGGSHMGGNYGDDRRGGRGGYDRGGY
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US-09-919-039-324
                                                                                                                                                                                                                                                           US-09-919-039-324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Kaser, Matthew R.
TITLE OF INVENTION: GENES EXPRESSED IN TRI
FILB REFERENCE: pA-0035 US
CURRENT APPLICATION NUMBER: US/09/919,039
CURRENT FILING DATE: 2002-09-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/222,113
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 401
SOFTWARE: PERL Program
SEQ ID NO 324
LENGTH: 462
                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 134; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 324, Application US/09919039 Patent No. 6727066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                         LENGTH: 46
TYPE: PRT
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6727066 1813444CD1
                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 98
TELECOMMUNICATION INFORMATION:
TELECHONE: 215-875-8383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 295 amino acids
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APPLICATION NUMBER: PCT/
FILING DATE: 19-MAY-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                               118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    297 PDNRGRGGGGFDRGGMSRGGRGGGRGGMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  237 PTSYPPQTGSYSQAPSQYSQQSSSYGQQSSFRQDHPSSMGYYGQBSGGFSGPGENRSMSG
 91
                                                              49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                            60 TYGQTAYATSYGQPP-TGYTTPTAPQAYSQPVQGYG-TGAYDTTTATVTTTQASYAAQSA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , 68
                                                                                                                                                          1 MASTDYSTYSQAAAQQGYSAYTAQFTQGYA-QTTQAYGQQSYGTYGQPTDVSYTQAQTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                            YGTQPAYPAYGQQPAATAPTRPQDGNKPTETSQPQSSTGGYNQPSLGYGQSNYSYPQVPG
                                                              GYGQSSY-SSYGQSQNTGYGTQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                             MASNDYT----QQATQSYGAYPTQPGQGYSQQSSQPYGQQSYSGYSQSTD-----TS
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YGQQSSYPGYGQQPA
                                                                                                                                                                                            Conservative
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                                                                                                                                                                                          Score 470.5; DB 4
Pred. No. 9.7e-25;
5; Mismatches 92
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Pred. No. 6.7e-26;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89
 - PSSTSGSYGSSS---QSSSYGQPQ-SG
                                                                                                                                                                                                                           DB 4;
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                                      Matches
                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: AEDIT 1.0 DOS text editor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/343,443B
FILING DATE: 18-NOV-1994
                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Thomas, G
APPLICANT: Zucman, J
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                FILING DATE: 20-MAY-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Weiser & Associates
STREET: 230 South Fifteenth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION
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                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 989.6121P
                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/
FILING DATE: 19-MAY-1993
                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                    NAME: Weiser, Gerard
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 19102
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                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                               TELEPHONE:
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363 IYVQGLNDSVTLDDLADFFKQCGVVKMNKRTGQPMIHIYLDKETGKPKGDATVSYEDPPT 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178 SYPMQPVTAPPSYPPTSYSSTQPTSYDQSSYSQQNTYGQPSSYGQQSSYGQQS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION:
                                      96;
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                                                                                                                                                           86 amino acida
                                                                                                                                                                                                                215-875-8394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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Ploougastel, Beatrice
Thomas, Gilles
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                                    Conservative
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                                                                                                                                                                                                                                                                                                   Gerard J
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                                                 12.5%; Score 453; DB 2;
100.0%; Pred. No. 2.2e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129
                                                                                                                                                                                                                                                                                                                                                      FR 92/06123
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                                  0,
                                    Mismatches
                                                                   Length 86;
                                    Indels
                                  0;
                                  Gaps
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US-08-963-825-21
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                                                                                                                                                                                  Matches 184;
                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Qvist,
APPLICANT: Bonde,
                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1078 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                        IMMEDIATE SOURCE: CLONE: COLLAGEN ALPHA 1 (III)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 21-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEPAX: 212-753-6237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 10022
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                              ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Gogoris, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             423 AKAAVEWFDGKDFQGSKLKVSLARKK 448
162 SL----
                                                                    102 TATVTTTQASYAAQSAYGTQPAYPAYGQQPAATAPTRPQDGNKPTETSQPQSSTGGYNQP 161
                                                                                                                                           42 GTYGQPTDVSYTQAQTTATYGQTAYATSYGQPPTGYTTPTAPQAYSQPVQGYGTGAYDTT 101
                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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                                                                                                                                                                                  Conservative
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-GYGOSNYSYPQ---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A Method for Assaying Collagen Fragments
in Body Fluids, A Test Kit and Means for
Method and Use of the Method to Diagnose
Disorders Associated with the Metabolism
                                                                                                                                                                                                 10.4%;
                                                                                                     -----GSPGSPGYQGPPGEP--GQAGPSGPPG---PPGAIG-----
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                                                                                                                                                                              ; Score 376.5; DB 3; ; Pred. No. 8e-18; 34; Mismatches 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4305/08701
                                    -GKDGESGRPGRPGDRGLP----GPPGIKGPAGIP
-VPGSY----PMQPVTAPPSYPPTSYSSTQ 199
                                                                                                                                                                                                                  Length 1078;
                                                                                                                                                                                  Indels
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RESULT 14
US-09-500-811-21
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                                                                                                                                                                                                                                                                                                                                                         Sequence 21, Application US/09500811
Patent No. 6323314
GENERAL INFORMATION:
APPLICANT: Qvist, Per
APPLICANT: Bonde, Martin
TITLE OF INVENTION: A Method for Assaying Collagen Fragments
TITLE OF INVENTION: Method and Use of the Method to Diagnose
TITLE OF INVENTION: Disorders Associated with the Metabolism
NUMBER OF ENURENCES: 21
CORRESPONDENCE ADDRESS: Darby & Darby PC
                                                                   CLASSIFICATION:
PRIOR APPLICATION NUMBER:
                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                 FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                      CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                            APPLICATION NUMBER: FILING DATE:
NAME: Gogoris, Adda REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                     ZIP: 10022
                                                                                                                                                                                                                                                                                                                                              STREET:
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 43
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEPAX: 212-753-6237
TELEX: 236687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1078 amino acid
TYPE: amino acid
TOPOLOGY: linear
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                                                                  RĞPQĞLQGLPĞTĞĞPPGENEKPGEPGPKGEAGAPĞAPĞĞKGDAĞAPĞERĞPPGLAGAPĞL
                                                                                                   GGMRG-----GRGGLMDR------GGPGGMFRGGRGGDRG------GF
                                                                                                                                                                        GNVQHRAGDWQCPNPGCGNQNFAWRTECNQCKAPKPEGFLPPPFPP----PGGDRGRGGP
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RGGAG-PPGPEGGKGAAGPPGPPGAAGTPGLQGMPGERGGLGSPGPKGDKGE
                                RGGRGMDRGGFGGGRRGGPPG----PLMEQMGGRRGGRGGPG-KMDKGE 646
                                                                                                                                       DGAPGKNGERGGPG-GPGPQG-----PPGKNGEYGPQGPPGPTGPGGDKGDTGP
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RESULT 15 US-09-570-573-21

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PATENT NO. 6342361
GENERAL INFORMATION:
GAPPLICANT: QViet, Per
APPLICANT: Bonde, Martin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 236687
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1078 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: COLLAGEN ALPHA 1 (III)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: GOGOTIS, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305/08701
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: A Method for Assaying Collagen Fragments
TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for Carrying Out the
TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of
TITLE OF INVENTION: Disorders Associated with the Metabolism of
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/570,573 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 10022
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    302
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                                                                                                                                   159
                                                                                                                                                                     200 PTSYDQSSYSQQNTYGQPSSYGQQSSYGQQSSYGQQPPTGTGSYSQASQYSQQSS 259
                                                                                                                                                                                                                                                                                                                                                  102 TATVTTTQASYAAQSAYGTQPAYPAYGQQPAATAPTRPQDGNKPTETSQPQSSTGGYNQP 161
                                                                                                                                                                                                                                                                                                         76 -----GPPGIKGPAGIP 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                            42 GTYGQPTDVSYTQAQTTATYGQTAYATSYGQPPTGYTTPTAPQAYSQPVQGYGTGAYDTT 101
                                                                                                                                                                                                                    GFPGMKGHRGFDGRNGEKGETGAPGLKGENGLPGENGAPGPMGPRGAP------
                                         EVGPAGS----PGSNGAPGQRGEPGPQGHAGAQGPPGPPGINGSPGGKGEMGPAGIPGA 259
                                                                                     SYGQQSSFRQDHPSSMGVYGQ--ESG--GFSG-----PGENRSMSGPDNRG-----
                                                                                                                              -----GERGRPGLPGAAGARGNDGARGSDGQPGPPG-PPGTAGPPGSPG----AKG 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               212-753-6237
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----RGRGGFDRGGMSRGGRGGGRGGMGSAGERGGFNKPGGPMDEGPDL 346
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OMGGRRGGRGGPG-KMDKGE 646	GGPGGMFRGGRGGDRGGF 599	CKAPKPEGF1PPPFPPPGGDRGRGGP 568	GPMGRMGGRGGDRGGFPPRGPRGSRGNPSGG 512	KLKVSLARKKPPMNSMRGGLPPREGR 464	DFFKQCGVVKWNKRTGQPMIHIYLDKET 406	: s s s s s s s s s s s s s s s

Search completed: February 18, 2005, 15:13:48 Job time : 50 secs

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Result
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Perfect score:
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Maximum Match 10
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seq length: 2000000000
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_NEW PUB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US08_NEW PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/US08_NEW PUB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

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Gapop 10.0 , Gapext 0.
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Listing first 45 summaries
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Copyright (c) 1993 - 2005 Compugen Ltd.
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15 US-10-094-749-2713
16 US-10-755-89-650
16 US-10-408-765A-116
17 US-09-925-301-151
18 US-09-919-039-324
19 US-09-919-039-324
10 US-09-919-039-324
10 US-09-918-715-226
115 US-10-437-963-191926
115 US-10-177-293-68
114 US-10-177-293-68
115 US-10-257-021-72
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Sequence 2, Appli
Sequence 2713, App
Sequence 650, App
Sequence 116, App
Sequence 1511, App
Sequence 42397, A
Sequence 191926,
Sequence 69744, App
Sequence 69744, App
Sequence 226, App
Sequence 33, Appl
Sequence 33, Appl
Sequence 33, Appl
Sequence 72, Appl
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-10-171-311-3	0-03	-09-918-715-26	-10-488-056-	-100	-09-861-597-1	-09-795-061-	-10-468-091-	-10-058-124-2	0-468-091-2	-10-468-091-2	-10-402-072A-	-10-402	-10-468-091-	-10-437-	-10-788-792-2	-10-468	-10-236-031B	-10-301-822-	-10-177-293-7	-10	0-40	-10-058	-10-402-072P	-10-402-089-1	-10-402	-10-402-072A-	US-10-402-089-6	US-10-402-089-4	US-10-734-564-103	-10-358-	US-10-357-851-3
e u	e 15	e 26	47	Sequence 10, Appl	10,	e 2,	e G	e 20	e 25	e 26	e 2,	e 2	e 23	e 164510,	e 248,	e 22, 1	e 74, App	35	e 70,	e 8,	æ	e 21,	12	12	е 6	4	е 6,	e 4,	e 103, Ap	е 3, Ap	Sequence 3, Appli

ALIGNMENTS

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Sequence 2, Application US/10791017A

Publication No. US20040197827A1

GENERAL INFORMATION:
APPLICANT: JENAPHARM GmbH & Co. KG
TITLE OF INVENTION: Methods for Determining Hormonal Effects of Substances
FILE REFERENCE: Pat 3684/11
CURRENT APPLICATION UNMEER: US/10/791,017A
CURRENT FILING DATE: 2004-03-02
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 656
TYPE: PRT
ORGANISM: Homo sapiens
US-10-791-017A-2
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Best Local Similarity
Matches 656; Conserv
181 MQPVTAPPSYPPTSYSSTQPTSYDQSSYSQQNTYGQPSSYGQQSSYGQQSYGQQPPTSY
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                                                                                                   121 QPAYPAYGQQPAATAPTRPQDGNKPTETSQPQSSTGGYNQPSLGYGQSNYSYPQVPGSYP 180
                                                                                                                                                                         61 YGQTAYATSYGQPPTGYTTPTAPQAYSQPVQGYGTGAYDTTTATVTTTTQASYAAQSAYGT 120
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APPLICANT: SEKI, NACHIKO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOYUKI
APPLICANT: MAGHARA, KENJI
APPLICANT: MAGHARA, KENJI
APPLICANT: MAGHARA, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR PILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOPTWARE: PATENTIN VET. 2.1
SEQ ID NO 2713
LENGTH: 600
TYPE: PRI
ORGANITSM: UTO GETTARE
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US-10-094-749-2713
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APPLICANT: ISOGAI, T.
APPLICANT: SUGIYAMA
APPLICANT: OTSUKI,
Query Match 90.2%;
Best Local Similarity 91.3%;
Matches 599; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2713, Application US/10094749 Publication No. US20030219741A1
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APPLICANT:
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OTSUKI, TETSUJI
WAKAMATSU, AI
SATO, HIROYUKI
ISHIZUKO
YAMAMOTO, JUN-ICHI
ISONO, YUUKO
                                                                                                                                                                                                                                                                                                                                                                                                                OTSUKA, KAORU
NAGAI, KEIICHI
IRIE, RYOTARO
TAMECHIKA, ICHIRO
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 Score 3277; DB 15;
Pred. No. 7.9e-188;
0; Mismatches 1;
                                 Length 600;
   Indels
   56;
   Gaps
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                 Query Match 35.3%; Score 1281.5; DB 16; Length 525; Best Local Similarity 44.8%; Pred. No. 1.1e-68; Matches 299; Conservative 59; Mismatches 155; Indels 155;
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RESULT 3
US-10-755-889-650

VS-quence 650, Application US/10755889

Publication No. US20040171823A1

GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-kB
TITLE OF INVENTION: PATHWAY
FILE REFERENCE: D0284 NP
CURRENT APPLICATION NUMBER: US/10/755,889
CURRENT FILING DATE: 2004-01-13
APRIOR APPLICATION NUMBER: U.S. 60/440,068
FRIOR APPLICATION NUMBER: U.S. 60/440,068
FRIOR FILING DATE: 2003-01-14
APRIOR FILING DATE: 2003-05-12
ANDMEER OF SEQ ID NOS: 823
SOPTWARE: PATENTIN VERSION 3.2
SEQ ID NO 650
LENGTH: 525
TYPE: PATT
ORGANISM: Homo sapiens
US-10-755-889-650
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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 Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being prand is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 0.5
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3633
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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             RNA-binding fus-like py RNA/ssDNA-lagen a. collagen a. glutenin h. collagen a. collagen a. glutenin a.
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ALIGNMENTS

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Oy 61 YGQTAYATSYGQPPTGYTTPTAPQAYSQPVQGYGTGAYDTTTATVTTTQASYAAQSAYGT 120	Query Match 100.0%; Score 3633; DB 1; Length 656; Best Local Similarity 100.0%; Pred. No. 3.9e-168; Matches 656; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 656; Conservative 0; Mismatches 0; Indels 0; Oy 1 MASTDYSTYSQAAAQQGYSAYTAQPTQGYAQTTQAYGQQSYGTYGQPTDVSYTQAQTTAT 60	A;Accession: SW8257 A;Molecule type: mRNA A;Residues: 1-556 A;Residues: 1-556 A;Cross-references: EMBL:X56899; NID:g547565; PIDN:CAA47350.1; PID:g31280 C;Genetics: A;Gene: GDB:EWSR1 A;Cross-references: GDB:135984; OMIM:133450 A;Cross-references: GDB:135984; OMIM:133450 A;Map position: 22q12.1-22q12.1 A;Introns: 5/1; 17/2; 34/3; 76/1; 138/2; 194/2; 265/1; 325/2; 338/1; 349/1; 388/3; 432/1. A;Note: EWSR1 region is exons 7-10 of this gene, called EWS in reference A49958; this region is exons 7-10 of this gene, called EWS in reference A49958; this region is carcinogenesis; nucleus; RNA binding; tandem repeat homology C;Reywords: carcinogenesis; nucleus; RNA binding; tandem repeat F;362-437/Domain: ribonucleoprotein repeat homology <rrm></rrm>	RNA-binding protein EWS - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004 C;Accession: A49358; S28257 R;Plougastel, B.; Zucman, J.; Peter, M.; Thomas, G.; Delattre, O. Genomics 18, 609-615, 1993 A;Title: Genomic structure of the EWS gene and its relationship to EWSR1, a site of tumor A;Title: Gene number: A49358; MUID:94140360; PMID:9307570 A;Accession: A49358 A;Reference number: A49358; MUID:94140360; PMID:9307570 A;Accession: A49358 A;Residuse: 1-656 cRES> A;Cross-references: UNIPROT:001844, EMBL:X72990; NID:9485838; PIDN:CAA51489.1; PID:98256: A;Cross-references: UNIPROT:001844, EMBL:X72990; NID:9485838; PIDN:CAA51489.1; PID:98256: A;Title: Gene fusion with an ETS DNA-binding domain caused by chromosome translocation ir A;Accession: S28257; MUID:92396239; PMID:1522903 A:Accession: S28257; MUID:92396239; PMID:1522903	RESULT 1

```
ANA-Dinding protein Ews - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A55726; S45007
R;Plougastel, B.; Mattei, M.G.; Thomas, G.; Delattre, O.
Genomics 23, 278-281, 1994
A;Title: Cloning and chromosome localization of the mouse Ews gene.
A;Reference number: A55726; MUID:95130099; PMID:7829090
A;Reference number: A55726; MUID:95130099; PMID:7829090
A;Recession: A56726; MUID:95130099; PMID:7829090
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                                                                                                MOPVTAPPSYPPTSYSSTOPTSYDOSSYSOONTYGOPSSYGOOSSYGOOSSYGOOPPTSY
                                                                                                                                                                                                                                                                              YGQTAYATSYGQPPTGYTTPTAPQAYSQPVQGYGTGAYDTTTATVTTTQASYAAQSAYGT
PPQTGSYSQAPSQYSQQSSSYGQQSSFRQDHPSSMGVYGQESGGFSGPGENRSMSGPDNR
                                                                                                                                                    QPAYPTYGQQPTATAPTRPQDGNKPAETSQPQSSTGGYNQPSLGYGQSNYSYPQVPGSYP
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Pred. No. 3.6e-165;
B; Mismatches 4;
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A;Ttle: Fusion of CHOP to a novel RNA-binding protein in human myxoid liposarcoma. A;Reference number: S33798; MUID:93288139; PMID:8510758
A;Accession: S33799
A;Molecule type: mRNA
A;Residues: 1-526 <CRO>
A;Cross references: UNIFROT:D35637; GB:S62140; NID:g386156; PIDN:AAB27102.1; PID:g386
A;Cross references: UNIFROT:D35637; GB:S62140; NID:g386156; PIDN:AAB27102.1; PID:g386
A;Cross references: UNIFROT:D35637; GB:S62140; NID:g386156; PIDN:AAB27102.1; PID:g386
A;Cross references: UNIFROT:D35637; RID:g386156; PIDN:AAB27102.1; PID:g386
A;Experimental source: liposarcoma
A;Reference number: S36157; MUID:g3350637; PMID:7503811
A;Accession: S36157
A;Gaccele type: mRNA
A;Residues: 1-63,'S',66-526 <RAB>
A;Cross references: EMB:X71428; NID:g333415; PIDN:CAA50559.1; PID:g4210363
A;Experimental source: liposarcoma
C;Genetics: A;Genetics: GDB:TUS
A;Gene: GDB:TUS
A;Gene: GDB:TUS
A;Gene: GDB:TUS
A;Gene: GDB:TUS
A;Gene: GDB:136048; OMIM:137070
A;Map position: RNA binding; probable plays a role in transcriptional regulation
C;Superfamily: RNA-binding protein, EWS type; ribonucleoprotein repeat homology
C;Keywords: carcinogenesis; nucleus; RNA binding; tandem repeat
F;286-361/Domain: ribonucleoprotein repeat homology <RRM>
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833799
RNA-binding protein FUS, nuclear - human
N,Alternate names: RNA-binding protein TLS
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S33799; S36157
R;CTOZAt, A.; Aman, P.; Mandahl, N.; Ron, D.
Nature 363, 640-644, 1993
Nature 363, 640-644, 1993
                                                                                                      Query Match
Best Local Similarity
Matches 301; Conserv
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MASNDYT----QQATQSYGAYPTQPGQGYSQQSSQPYGQQSYSGYSQSTD-----TS
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                                                                                                        Conservative
                                                                                                                                 35.3%;
                                                                                                      59;
                                                                                                      Score 1282; DB 1;
Pred. No. 4.7e-55;
9; Mismatches 153;
                                                                                                                                                    Length 526;
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TYGQTAYATSYGQPP-TGYTTPTAPQAYSQPVQGYG-TGAYDTTTATVTTTQASYAAQSA 117

Title: Perfect score: Sequence:

Scoring table:

Searched:

Run on:

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Gapop 10.0 , Gapext 0.5
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3633
1 MASTDYSTYSQAAAQQGYSA......GGPGKMDKGEHRQERRDRPY 656
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Copyright (c) 1993 - 2005 Compugen Ltd.
DB
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QSNVA3
EWS MOUSE
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          Q6DKB4
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Q6dkb4 xenopus lae
Q8cfq9 mus musculu
P35637 homo sapien
Q8tbr3 homo sapien
Q13344 homo sapien
Q8bq46 mus musculu
Q92804 homo sapien
Q95kg8 macaca fasc
Q86x94 homo sapien
Q6gld1 xenopus tro
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Opers6 brachydanio
Opbwa2 homo sapien
O803e3 brachydanio
O803e3 brachydanio
O80407 brachydanio
O905d1 homo sapien
O614y8 gallus gall
O72xq2 xenopus lae
O28009 bos taurus
P56959 mus musculu
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Q6nva3 mus musculu
Q61545 mus musculu
Q9d2p0 mus musculu
Q9daph homo sapien
Q6p3n0 xenopus tro
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Regult No.

Score

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Database

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113	1466	1163	394	101	414	265	448	280	189	442	399	410	475
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Q8BQU4	CA13_HUMAN	Q8N6U4	Q6YS82	Q98UE8	Q69TN3	Q6DDA7	Q18265	Q91VQ2	Q71E78	Q7PUK2	CAZ_DROME	Q7ZUE3	Q66J39
Q8bqu4	P02461	Q8n6u4	Q6ys82	Q98ue8	Q69tn3	Q6dda7	Q18265	Q91vq2	Q71e78	Q7puk2	Q27294	Q7zue3	Q66j39
mus musculu	homo sapien	homo sapien	oryza sativ	xenopus lae	oryza sativ	xenopus tro	caenorhabdi	mus musculu	homo sapien	anopheles g	drosophila	brachydanio	xenopus lae

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ALTERNATIVE SPLICING, AND KWA-______
ALTERNATIVE SPLICING, AND KWA-_____
MEDLINE=94366763; PubMed=8084618;
MEDLINE=94366763; PubMed=8084618;
Ohno T., Ouchida M., Lee L., Gatalica Z., Rao V.N., Reddy K.S.E.,
Ohno T., Ouchida M., Lee L., Gatalica Z., Rao V.N., Reddy K.S.E.,
Ohno T., Ouchida M., Lee L., Gatalica Z., Rao V.N., Reddy K.S.E.,
Ohno T., Ouchida M., Lee L., Gatalica Z., Rao V.N., Reddy K.S.E.,
Ohno T., Ouchida M., Lee L., Gatalica Z., Rao V.N., Reddy K.S.E.,
Ohno T., Ouchida M., Lee L., Gatalica Z., Rao V.N., Reddy K.S.E.,
Ohno T., Ouchida M., Lee L., Gatalica Z., Rao V.N., Reddy K.S.E.,
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Ohno T., Ouchida M., Lee L., Gatalica Z., Rao V.N., Reddy K.S.E.,
Ohno T., Children M., Children M., Reddy K.S.E., Reddy K.S.E.,
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Ohno T., Children M., Children M., Reddy K.S.E., Reddy K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20390060; PubMed=10767297; DOI=10.1074/jbc.M002961200; Li K.K.C., Lee K.A.W.; "Transcriptional activation by the Ewing's sarcoma (EWS) oncogne cis-repressed by the EWS RNA-binding domain."; J. Biol. Chem. 275:23053-23058(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98325009; PubMed=9660765; DOI=10.1074/jbc.273.29.18086; Zhang D., Paley A.J., Childs G.; "The transcriptional repressor ZPM1 interacts with and modulate ability of EWS to activate transcription."; J. Biol. Chem. 273:18086-18091(1998).
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"Exposure on cell surface and extensive arginine methylation of Ewing sarcoma (EWS) protein.";
J. Biol. Chem. 276:18681-18687(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 128-158; 233-247; 268-324; 334-364; 393-439; 447-518 551-641, METHYLATION OF ARGININES, AND MASS SPECTROMETRY. MEDLINE-21276345, Pubmed-11278906; DOI=10.1074/jbc.M011446200; Belyanskaya L.L., Gehrig P.M., Gehring H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHOSPHORYLATION SITE SER-266, AND PARTIAL SEQUENCE.

MEDLINE=98001723; PubMed=9341188; DOI=10.1074/jbc.272.43.27369;

Deloulne J.C., Prichard L., Delattre O., Storm D.R.;

"The prooncoprotein EWS binds calmodulin and is phosphorylated!

protein kinase C through an IQ domain.";

J. Biol. Chem. 272:27369-27377(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Identification of new members
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Zucman-Rossi J., Legoix P., Thomas G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHARACTERIZATION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schnerch A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fusion pa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fusion protein target genes. SUBUNIT: Binds POLR2C, SF1, calmodulin and RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: Might normally function as a repressor. EWS-fusion-proteins (EFPS) may play a role in the tumorigenic process. They may disturb gene expression by minicking, or interfering with the normal function of CTD-POLII within the transcription initiation complex. They may also contribute to an aberrant activation of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mouse cDNA sequences.";
c. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                            ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Nuclear,
                                                                                            Name=EWS-B
                                                                                                                                                                                                                                     Event=Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chromosomes Cancer 13:126-132(1995)
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                                                                                                                                        IsoId=Q01844-1;
                                           IsoId=Q01844-2; Sequence=VSP_005793;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schein J.E., Jones S.J.M., Marra M.A.; and initial analysis of more than 15,000
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experimental confirmation available;
                                                                                                                                                                                                                                                                                 from cytoplasm
/E PRODUCTS:
                                                                                                                                        Sequence=Displayed;
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                                                                                                                                                                                                                                     isoforms=2;
                                                                                                                                                                                                                                                                                                                                  PTK2B/FAK2
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             are thought to arise via EFP-induced transcriptional deregulation, with the tumor phenotype specified by the EWSRI fusion partner and cell type. Transcriptional repression of the transforming growth factor beta type II receptor (TGF beta RII) is an important target of the EWS-FLI1, EWS-ERG, or EWS-ETV1 oncogene.

MISCELLANEOUS: Binds calmodulin in the presence, but not in the absence, of calcium ion.

SIMILARITY: Belongs to the RNP TET family.

SIMILARITY: Contains 1 RQ domain.

SIMILARITY: Contains 1 RANEP2-type zinc finger.

SIMILARITY: Contains 1 RANEP2-type zinc finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    activation domain in EPPS. EWSR1 binds POLR2C but not POLR2E POLR2C, whereas the isolated EAD binds POLR2E and POLR2G but pot POLR2C. Cis-linked RNA-binding domain (RBD) can strongly and specifically repress trans-activation by the EAD.

PMM: Phosphorylated; calmodnlin-bindin--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      involves EWSR1 and WT1.

DISEASE: Malignant melanoma of soft parts (MMSP), also know soft tissue clear cell sarcoma, is a rare tumor developing tendons and aponeuroses. It is associated with chromosomal translocation t(12;22)(q13;q12) involving EWSR1 and ATF-1.

DISEASE: Involved in small round cell sarcoma through a chromosomal translocation t(1;22)(p36.1;q12) that involves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISEASE: Ewing's sarcoma is characterized by chromosomal translocations t(1;22)(q24,q12) which involves EWSR1 and FLI1, t(7;22)(q22,q12) which involves EWSR1 and ETV1, t(21;22)(q22,q12) which involves EWSR1 and ERG and t(9;22)(q22-31;q11-12) which involves EWSR1 and ERG and t(9;22)(q22-31;q11-12) which involves EWSR1 and NR4A3.

DISEASE: Involved in desmoplastic small round cell tumor (DSRCT) through a chromosomal translocation t(11;22)(p13;q12) that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   which EWSR1 is fused to a variety of cellular transcription factors. RPPS are very potent transcriptional activators dependent on the EAD and a C-terminal DNA-binding domain contributed by the fusion partner. The spectrum of malignancies associated with EPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE SPECIFICITY: Ubiquitous.
DOMAIN: EWS activation domain (EAD)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and ZNF278.
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4; CAAS1489.1; JOINED.

95; CAAS1489.1; JOINED.

996; CAAS1489.1; JOINED.

2997; CAAS1489.1; JOINED.

2998; CAAS1489.1; JOINED.

72999; CAAS1489.1; JOINED.

73000; CAAS1489.1; JOINED.

X73001; CAAS1489.1; JOINED.

X73002; CAAS1489.1; JOINED.

X73003; CAAS1489.1; JOINED.

X73004; CAAS1489.1; JOINED.

4; X73004; CAAS1489.1; JOINED.

51; BC004817; AAH04817.1; -...

91; Y08806; CAA70044.1; ALT_INJ

91; Y08806; CAA70044.1; ALT_INJ

91; Y08806; CAA70044.1; -...
A49358; A49358.
; O95218; 1NOZ.
                                                                                                                                                                                             X72991;
X72992;
X72993;
X72994;
X72995;
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X72990;
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Best Local Similarity
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Q96FE8;
Q96FE8;
01-DEC-2001
01-DEC-2001
25-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H-InvDB; HIX0016349;
MIM; 133450; -.
                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                  Ewing sarcoma breakpoint Name=EWSR1;
                                                                                                       NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                    GGRGMDRGGFGGGRRGGPGGPPGPLMEQMGGRRGGRGGPGKMDKGEHRQERRDRPY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MASTDYSTYSQAAAQQGYSAYTAQPTQGYAQTTQAYGQQSYGTYGQPTDVSYTQAQTTAT
                                                                                                                                                            (TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 28, Last annotation update)
ma breakpoint region 1, isoform EWS (EWS
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                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                   Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Submitted (
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RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Browmstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Browmstein M.J., Disdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., WcEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length human

Tand mouse cDNA sequences ";

The Decomposition of the Property of t
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Pfam; PF00076; RRM 1; 1.—
Pfam; PF00641; zf-RanBP; 1.

PIRSF; PJRSF002101; RNA-binding_EWS; 1

SMART; SM00360; RRM; 1.

SMART; SM00547; znF RBZ; 1.

SMART; SM00547; znF RBZ; 1.

PROSITE; PS50102; RRM; 1.

PROSITE; PS501358; ZF RANBP2 1; 1.

PROSITE; PS50139; ZF RANBP2 2; 1.

PROSITE; PS5019; ZF RANBP2 2; 1.

PROSITE; PS50199; ZF RANBP2 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; 095218; 1N0Z.

GO; GO:0003634; C:nucleus; IEA.

GO; GO:0003676; F:nucleic acid binding; IEA.

GO; GO:0008270; F:zinc ion binding; IEA.

InterPro; IPR011368; RNA-binding_EWS.

InterPro; IPR000504; RNA rec_mot.

InterPro; IPR001504; RNA rec_mot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Beare D.M., Dunham I.;
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases
EMBL; BC011048; AAH11048.1; -.
EMBL; BC072442; AAH72442.1; -.
EMBL; CR456490; CAG30376.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Collins J.E., wright
Cole C.G., Goward M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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PPQTGSYSQAPSQYSQQSSSYGQQSSFRQDHPSSMGVYGQESGGFSGPGENRSMSGPDNR
                                                                                                                QPAYPAYGQQPAATAPTRPQDGNKPTETSQPQSSTGGYNQPSLGYGQSNYSYPQVPGSYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MASTDYSTYSQAAAQQGYSAYTAQPTQGYAQTTQAYGQQSYGTYGQPTDVSYTQAQTTAT
                                                                        MOPVTAPPSYPPTSYSSTOPTSYDOSSYSOONTYGOPSSYGOOSSYGOOSSYGOOPPTSY
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Pred. No. 1.1e-147;
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               RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Haysahi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Tanai H., Kimata M., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
RA Musashino K., Yuuki H., Oshima A., Sasaki N., Acteuka S.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Makagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Yujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Pujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA RA Pujimori Y., Komiyama M., Tashiro M., Ohmori Y.,
RA Kawabata A., Hikiji T., Nobateke N., Inagaki H., Ikema Y., Okamoto S.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,
Tonaka T., Nakamura Y., Ohara O., Isogai T., Sugano S.,
Tonaka M., Takama M., Takama N., Takahashi Y., Nakagawa K.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,
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Q96MX4;
01-DEC-2001
01-DEC-2001
01-MAR-2004
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein FLJ31747.
Homo sapiens (Human).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Best Local Similarity
Matches 655; Conserv
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EMBL; AKD56309; BAB71145.1; -.

HSSP; O95218; 1NOZ.

GO; GO:0005634; C:nucleus; IEA.

GO; GO:0005636; F:nucleic acid binding; IEA.

GO; GO:0003676; F:zinc ion binding; IEA.

InterPro; IPR011368; RNA-binding EWS.

InterPro; IPR011368; RNA-rec_mot.

InterPro; IPR010504; RNA, rec_mot.

InterPro; IPR001876; Znf_RanGDP.

Pfam; PF00076; RRM 1; I.

Pfam; PF00076; RRM 1; I.

SMART; SM00360; RRM; 1.

SMART; SM00360; RRM; 1.

PROSITE; PS01138; ZP RANBP2 1; 1.

PROSITE; PS01199; ZF RANBP2 1; 1.

PROSITE; PS01199; ZF RANBP2 2; 1.

SEQUENCE 661 AA; 68966 MW; 5F84F52FDCD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGPDNRGRGGGFDRGGMSRGGRGGGRGGMGSAGERGGFNKPGGPMDEGPDLDLGPPVDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YGQTAYATSYGQPP-----
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                                                                                                                                                                                                                                                                                                                                        AWRTECNQCKAPKPEGFLPPPFPPPGGDRGRGGPGGMRGGRGGLMDRGGPGGMFRGGRGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEDSDNSAIYVQGLNDSVTLDDLADFFKQCGVVKMNKRTGQPMIHIYLDKETGKPKGDAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QPPTSYPPQTGSYSQAPSQYSQQSSSYGQQSSFRQDHPSSMGVYGQESGGFSGPGENRSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VPGSYPMQPVTAPPSYPPTSYSSTQPTSYDQSSYSQQNTYGQPSSYGQQSSYGQQSSYGQ
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Pred. No. 4.2e.
0; Mismatches
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C. STRAIN-ECSTBL/6; TISSUE-Brain,
C. A. Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
C. A. Alteschul S.F., Zebeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
C. A. Alteschul S.F., Zebeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
C. A. Alteschul S.F., Jordan H., Moore T., Mass S.I., Wang J., Hsleh F.,
C. A. Alteschul S.F., Jordan H., Moore T.A., Rubin G.M., Hong L.,
C. A. Brownstein M.J., Dadin T.B., Toshiyuki S., Carrinci P., Prange C.,
C. A. Stepleton M.J., Usdin T.B., Toshiyuki S., Carrinci P., Prange C.,
C. A. Stepleton M.J., Usdin T.B., Toshiyuki S., Carrinci P., Prange C.,
C. A. Blows S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
C. A. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullahy S.J.,
C. A. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullahy S.J.,
C. A. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J.,
C. A. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J.,
C. A. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J.,
C. A. Richards S., Worley K.C., Shevchenko Y., Bouffard G.G.,
C. A. Milting M., Touchman J.W., Green E.D., Dickeon M.C.,
C. A. Krzywinski M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.B.,
C. A. Krzywinski M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.B.,
C. A. Krzywinski M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.B.,
C. A. Krzywinski M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.B.,
C. A. Krzywinski M. I., Skalska U., Smailus D.B., Schnerch A., Schein J.B.,
C. A. Krzywinski M. I., Skalska U., Smailus D.B., Schnerch A., Schein J.B.,
C. A. Krzywinski M. I., Skalska U., Smailus D.B., Schein J.B.,
C. A. Krzywinski M. I., Skalska U., Smailus D.B., Schein J.B.,
C. A. Krzywinski M. I., Skalska U., Smailus D.B., Sc
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Best Local S
Matches 642
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Director MGC Project;
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC068226; AAH68226.1; -.
GO; GO:0005634; C:nucleus; IDA.
InterPro; IPR011368; RNA-binding_EWS.
InterPro; IPR001504; RNA rec mot.
InterPro; IPR001504; RNA rec mot.
InterPro; IPR001576; Znf_RanGDP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00360; RRM; 1.

SMART; SM00547; ZnP RBZ; 1.

PROSITE; PS50102; RRM; 1.

PROSITE; PS501358; ZP RANBP2 1; 1.

PROSITE; PS50199; ZP RANBP2 2; 1.

SEQUENCE 656 AA; 68549 MW; 5D!
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Pfam, PF00641; zf-RanBP; 1.
PIRSF, PIRSF002101; RVA-binding_EWS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000
"Generation and colla sequences.";
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name-Ewerl;
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           181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                             MASTDYSTYSQAAAQQGYSAYTAQPTQGYAQTTQAYGQQSYGTYGQPTDVSYTQAQTTAT
MQPVTAPPSYPPTSYSSTQPTSYDQSSYSQQNTYGQPSSYGQQSSYGQQSSYGQQPPTSY, 240
                                                                             QPAYPTYGQQPTATAPTRPQDGNKPAETSQPQSSTGGYNQPSLGYGQSNYSYPQVPGSYP
                                                                                                                        QPAYPAYGQQPAATAPTRPQDGNKPTETSQPQSSTGGYNQPSLGYGQSNYSYPQVPGSYP
                                                                                                                                                                                                                         YGQTAYATSYGQPPTGYSTPTAPQAYSQPYQGYGTGTYDSTTATVTTTQASYAAQTAYGT
                                                                                                                                                                                                                                                                    YGQTAYATSYGQPPTGYTTPTAPQAYSQPVQGYGTGAYDTTTATVTTTQASYAAQSAYGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 3579; DB 2;
Pred. No. 5.6e-146;
9; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDF018A22C8C1D0B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 656;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plougastel B., Mattei M.-G., Thomas G., Delattre O.; "Cloning and chromosome localization of the mouse Ews gene."; "Genomics 23:278-281(1994).
-I- FUNCTION: Might function as a repressor (By similarity).
-I- SUBUNIT: Binds RNA, POLR2C, SF1 and calmodulin. Interacts with
                                                                                                                                                                                                        PTM: Phosphorylated; calmodulin-binding inhibits phosphorylation of Ser-266 (By similarity).

MISCELLANEOUS: Binds calmodulin in the presence, but not in the absence, of calcium ion (By similarity).

SIMILARITY: Belongs to the RNP TET family.

SIMILARITY: Contains 1 IQ domain.

SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
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R HSSP; 055218; 110Z.

R MGD; MGI:99960; Ewsh.

R GG; GO:0005634; C:nucleus; IDA.

R GG; GO:0005634; C:nucleus; IDA.

R InterPro; IPR000048; IQ region.

R InterPro; IPR000504; RNA rec_mot.

InterPro; IPR000504; RNA rec_mot.

R InterPro; IPR000504; RNA rec_mot.

R Pfam; pP00076; RNA j.l.

R Pfam; pP00076; RNA binding EwS; 1.

R PFRSF; PIRSF002101; RNA_binding EwS; 1.

R PROSITE; PS50102; RRM; 1.

R PROSITE; PS50102; RRM; 1.

R PROSITE; PS501358; ZF_RANBP2 1; 1.

R PROSITE; PS50199; ZF_RANBP2 1; 1.
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                     QPAYPAYGQQPAATAPTRPQDGNKPTETSQPQSSTGGYNQPSLGYGQSNYSYPQVPGSYP
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Asymmetric dimethylargining similarity).

Phosphoserine (by PKC) (By PKC) (By S0735EDB54247D69 CRC64;
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Pred. No. 1.2e-145;
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                                                                                SEQUENCE FROM N.A.

STRAIN-C57BL/6J; TISSUE-Placenta and extra embryonic tissue;

MEDLINE-20499374, PubMed-11042159, DOI-10.1101/gr.145100;

Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., It

Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

"Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new ge

Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9D2P0 PRELIMINARY; PRT; 655 AA.
Q9D2P0; 17EMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 18 days pregnant adult female placenta and extra
embryonic tissue cDNA, RIKEN full-length enriched library,
clone:3830417B11 product:Ewing sarcoma homolog, full insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=C57BL/6J; TISSUE=Placenta The FANTOM Consortium,
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STRAIN-C57BL/6J; TISSUE-Placenta and extra embryonic tissue;
MEDLINE-21085660; PubMed-11217851; DOI-10.1038/35055500;
RIKEN FANTOM Consortium;
        SEQUENCE FROM N.A. STRAIN=C57BL/6J; T
                                                                                                                                                                                                                                                                                                                                                        the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annot 60,770 full-length cDNAs."; Nature 420:563-573(2002).
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STRAIN-C57BL/6J; TISSUE-Placenta and extra embryonic tissue;
MEDLINE-99279253; PubMed-10349636; DOI-10.1016/S0076-6879(99)03004-9;
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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        TISSUE-Placenta
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Rodentia;
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        embryonic tissue
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2 STRAIN=578L/6J; TISSUE=Placenta and extra embryonic tissue;

24 Adachi J., Alzawa K., Akahira S., Akimura T., Arai A., Aono H.,

25 Arakawa T., Bono H., Carninci P., Pukuda S., Fukunishi Y., Furuno M.,

26 Arakawa T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,

27 Al Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,

28 Arakawa T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,

29 Akatsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,

20 Akazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai K.,

20 Acazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai K.,

20 Acazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai K.,

20 Acazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai K.,

21 A. Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai K.,

22 A. Okazaki Y., Okido T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,

23 Ano H., Sazuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,

24 A. Sogabe Y., Suzuki H., Tagami R., Takahashi F., Tanaka T.,

25 A. Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,

26 A. Sogabe Y., Suzuki H., Tagami M., Tagawa A., Yoshino M.,

27 A. Muramatsu M., Hayashizaki Y.,

28 A. Muramatsu M., Hayashizaki Y.,

29 Akuramatsu M., Hayashizaki Y.,

20 Akuramatsu M., Hayashizaki Y.,

20 Akuramatsu M., Hayashizaki Y.,

20 Akuramatsu M., Hayashizaki Y.,

21 A. Migali M., Hayashizaki Y.,

22 A. Muramatsu M., Hayashizaki Y.,

23 Akuramatsu M., Hayashizaki Y.,

24 A. Matsunatsu M., Hayashizaki Y.,

25 A. Matsunatsu M., Hayashizaki Y.,

26 A. Matsunatsu M., Hayashizaki Y.,

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21 A. Matsunatsu M., Hayashizaki Y.,

22 A. Matsunatsu M., Hayashizaki Y.,

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24 A. Matsunatsu M., Hayashizaki Y.,

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Pfam; PF00076; RRM 1; 1.

Pfam; PF00641; zf-RanBP; 1.

PIRSF; PIRSF002101; RNA-binding_EWS; 1.

SMART; SM00360; RRM; 1.

SMART; SM00367; ZnF_RBZ; 1.

PROSITE; PS50102; RRM; 1.

PROSITE; PS01358; ZF_RANBPZ_1; 1.

PROSITE; PS01358; ZF_RANBPZ_2; 1.

SEQUENCE 655 AA; 68462 MW; 10C7F06;
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GO; GO:0005634; C:nucleus; IDA.
InterPro; IPR011368; RNA-binding_EWS.
InterPro; IPR005504; RNA_rec_mot.
InterPro; IPR001876; Znf_RanGDP.
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                                                                                                                    GRGRGGFDRGGMSRGGRGGGRGGAGSAGERGGFNKPGGPMDEGPDLDLGPPVDPDEDSDN
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97.7%;
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Length Indels

56;

120 60

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RX Pubmed-1470203; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamihara K., Katsuta N., Satok K., Fujimori K.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA Tanai H., Kimata M., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Moriya S., Momiyama H., Ichhara T., Shinata N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yumazaki M., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Matsumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Minura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Minura K., Nagase T., Nakayima N., Takhahashi Y., Nakagawa K.,
RA Makai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,
RA Makai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,
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Q96MN4; 19, Crea
01-DEC-2001 (TrEMBLrel. 19, Last
01-DEC-2001 (TrEMBLrel. 26, Last
01-MAR-2004 (TrEMBLrel. 26, Last
Hypothetical protein FLJ32119.
Homo aspiens (Human)
Eukharyota; Metazoa; Chordata; Cr
Mammalia, Eutheria; Primates; Ca
                                                                                                                                                                                                                                 "Complete sequencing CDNAs.";
                                                                                                                                                                                                               Nat. Genet.
GO:000534; C:nucleus; IEA.
GO:0003676; F:nucleic acid binding;
GO:0008270; F:zinc ion binding; IEA.
cerPro; IPR011368; RNA-binding EWS.
cerPro; IPR000504; RNA rec_mot.
terPro; IPR001876; Znf_RanGDP.
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095218; 1N0Z.
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                                                                                                                                                                                                          36:40-45 (2004) .
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(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
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Best Local Similarity
Matches 599; Conserv
                                                                                                       O5-VUL-2004 (TrEMBLrel. 27, Las 05-VUL-2004 (TrEMBLrel. 27, Las 05-VUL-2004 (TrEMBLrel. 27, Las Hypothetical protein MGC76258. Name=MGC76258;
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Pfam; PF00641; zf-RanBP; 1.
PIRSF; PIRSF002101; RNA-binding_EWS; 1.
SMART; SM00360; RRM; 1.
SMART; SM00547; ZnF_RBZ; 1.
PROSITE; PS50102; RRM; 1.
PROSITE; PS01358; ZF_RANBPZ_1; 1.
PROSITE; PS0199; ZF_RANBPZ_2; 1.
SEQUENCE 600 AA; 62478 MW; 1572CEB
                                                                                                                                                                             Q6P3N0
Q6P3N0;
05-JUL-2004
05-JUL-2004
05-JUL-2004
     Xenopus tropicalis (Western clawed frog) ((Eukaryota; Metazoa; Chordata; Craniata; Venamphibia; Batrachia; Anura; Mesobatrachia; Xenopodinae; Xenopus.
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YSTGAQQQYSSQQQYSSQQQYSTAQQX
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                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                27, Created)
27, Last sequence up
27, Last annotation
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Pred. No. 4.4e-133;
0; Mismatches 1;
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                                                                             (Silurana tropicalis).
Vertebrata; Euteleostomi;
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VYGQESGGFSGPGENRSMSGPDNR

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X Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
X Klausner R.D., Collins P.S., Wagner L., Shemmen C.M., Schuler G.D.,
X Allachul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
X Allachul S.F., Zeeberg B., Buerow R.A., Rubin G.M., Hsieh F.,
X Allachul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
X Allachul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
X Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
X Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
X Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
X Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
X Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
X Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
X Robak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
X Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
X Allalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
X Allalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
X Allalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
X Allachul M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
X Allachul M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
X Allachul M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
X Allachul M. I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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Matches 497;
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Best Local
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Pfam; PP00641; Zf-RanBp; 1.

SMART; SM00360; RRW, 1.

SMART; SM00547; ZnF RBZ; 1.

PROSITE; PS001012; PHOSPHOPANTETHEINE; UNKNOWN_1.

PROSITE; PS011358; ZF-RANBP2_1; 1.

PROSITE; PS01358; ZF-RANBP2_2; 1.

PROSITE; PS01358; ZF-RANBP2_2; 1.

SEQUENCE 674 AA; 71082 MW; C4E34C7B95449E0D (SEQUENCE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Klein S., Gerhard D.S.,

Klein S., Gerhard D.S.,

Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, BC063928, AAH63928.1; -.

InterPro; IPR0005162; Ppantne S.

InterPro; IPR00504; RNA rec mot.

InterPro; IPR001876; Znf_RanGDP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.
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                                                                                                                                                                                                                                                                                                                                                                                                 TYGQTAYATSYGQPPTGYTTPTAPQAYSQPVQGYGTGAYDTTTATVTTTQASYAAQSAYG
NKPGGPMDEGPDLDLGP-----PVDPDEDSDNSAIYVQGLNDSVTLDDLADFFKQCGVV, 387
                                           KSPYGQEPHQGFSSSGENRGSGGSDSRSRGRGMFERGGMSRGGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MASTDYSTYSQAAAQQGYSAYTAQPTQGYAQTTQA-YGQQSYGTYGQPTDVSYTQAQTTA
                                                                                                                                                                                                                                                                                                                                                                         SYGQSAYATSYGQPPTGYTAPAAPQAYSQPMQGYGSTGYDSTTATTTTTQATYAAPSAYG
                                                                  MGVYGQE-SGGESGPGENRSMSGPDNRGRGRGGFDRGGMSRGGRGGGRGGMGSAGERGGF
                                                                                                                        QQSGYGQQSSYQAPPQQQQPPPTSYPPPSSSYSSQPPGQYGQQSSSYGQQSSYRPDHSSS
                                                                                                                                                               QQSSYGQQSSY-----GQQPPTSYPPQTGSY-SQAPSQYSQQSSSYGQQSSFRQDHPSS
                                                                                                                                                                                                        PMQQVSAPPSYPPTSYSSSQTSSYEQSSYSQPSSYTQQSGYGQQASYSQQSSYGQPSSYG
                                                                                                                                                                                                                                                 PMQPVTAPPSYPPTSYSSTQPTSYDQS------SySQQNTYGQPSSYG
                                                                                                                                                                                                                                                                                          SQPAYPSYGQQPATTASARPQDGSKPADTSQPPPSTASYAQPSMGYSQSSYSYPQVPASY
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71.8%;
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A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casvant T.L., Scheetz T.E.,

B Stapleton M., Soares M.B., Bonaldo M.F., Casvant T.L., Scheetz T.E.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Hilalon D.K., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

A Hilalon D.K., Madan A., Young A.C., Shevchenko Y. Bouffard G.G.,

A Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

B Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

B Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

B Hakesley R.W., Touchman J.W., Schmutz J., Myers R.M., Butterfield Y.S.,

A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
EMBL; BC075120, AAH75120.1; -..
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003676; F:nucleic acid binding;
GO; GO:0008270; F:zinc ion binding; IEA.
InterPro; IPR006162; Ppantne S.
InterPro; IPR011368; RNA-binding_EWS.
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25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
45-OCT-2004 (TrEMBLrel. 28, Last sequence update)
45-OCT-2004 (TrEMBLrel. 28, Last sequence update)
45-OCT-2004 (TrEMBLrel. 28, Created)
45-OCT-2004 (TrEMBLrel. 28, Created)
45-OCT-2004 (TrEMBLrel. 28, Last sequence update)
45-OCT-2004 (TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jones S.J., Marra M.A.;
Jones S.J., Marra M.A.;
Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                         Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases
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PEam; PF00076; RRM 1; 1.

PIRSF; PIRSF002101; RNA-binding_EWS; 1.

SMART; SM00360; RRM; 1.

SMART; SM00547; ZnF RBZ; 1.

SMART; SM00547; ZnF RBZ; 1.

PROSITE; PS00102; PHOSPHOPANTETHEINE; UNKNOWN_1.

PROSITE; PS001358; ZF_RANBP2_1; 1.

PROSITE; PS01358; ZF_RANBP2_1; 1.

PROSITE; PS01358; ZF_RANBP2_2; 1.
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 Q6NUX1;
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IPR001876; Znf_RanGDP.
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                                            PRELIMINARY;
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Pfam; PF000761; zf-RahBP; 1.

SMART; SM00360; RRM; 1.

SMART; SM00367; ZnF RBZ; 1.

PROSITE; PS0102; RRW; 1.

PROSITE; PS01025; SUGAR TRANSPORT_1; UNKNOWN_1.

PROSITE; PS01358; ZF_RANBP2_1; 1.

PROSITE; PS01358; ZF_RANBP2_2; 1.

SEQÜENCE 624 AA; 64731 MW; D0113DF02861F221 CH
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii, Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
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Submitted (APR-2004) to the EMBL/GenBank/DDBJ
EMBL; BC066397; AAH68397.1; -.
ZFIN; ZDB-GENE-030131-2317; wu:fc04c01.
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TISSUE=Embryo;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pna8.242603899;
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Wu:fc04c01 protein (Fragment).
ORFNames=wu:fc04c01;
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InterPro; IPR005829; Sug_transporter.
InterPro; IPR001876; Znf_RanGDP.
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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166
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                                                                    SYPQVPGSYPMQPVTAPPSYPPTSYSSTQPTSYDQSSYSQQNT----YGQPSSYGQQSSYG
                                                                                                                                                                                                          SYAAQSAYGTQAAYAAYGQQAAATAATRAQDGNKATETSQAQSSTGGYNQASLGYGQSNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51.9%; Score 1885.5; DB 2; 56.7%; Pred. No. 1.7e-73; tive 70; Mismatches 117;
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- QQSTYSQQQQGGYQGQQGGYGQQSSYS
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RESULT

QGCRS5

ID CRS5

ID CRS5

ID CRS6

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SEQUENCE FROM N.A.
STRAIN-C57BL/6J, TISSUB-Head;
STRAIN-C57BL/6J, TISSUB-Head;
MEDLINE-99279253; PubMed=10349636; DOI=10.101
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9CRS5;
Q9CRS5;
01-JUN-2001
01-JUN-2001
01-MAR-2004
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Head;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                Nature
[3]
                                                                                                                                                                                           RIKEN FANTOM Consortium; "Functional annotation of a full-length Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 17 days embryo head cDNA, RIKEN full-length
library, clone:3300002D11 product:Ewing sarcoma homolog,
SEQUENCE FROM N.A. STRAIN-C57BL/6J; T
                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Head;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence.
                                                   the RIKEN Genome Exploration Research Group "Analysis of the mouse transcriptome based 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=Ewsrl; Synonyms=Ewsh;
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                                                                                                                            FANTOM Consortium,
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Rodentia;
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Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                 DOI=10.1038/35055500;
                                                                                                                                                                                                                                                                                                                                                                             DOI=10.1016/S0076-6879(99)03004-9;
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on functional
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; Murinae; Mus
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Best Local S
Matches 328
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MGD; MGI:99960; Ewsrl.
GO; GO:0005634; C:nucleus; IDA.
InterPro; IPR000504; RNA rec mot.
InterPro; IPR001876; Znf_RanGDP.
Pfam; pP00076; RRM 1; 1.
Pfam; pP00076; RRM 1; 1.
SMART; SM00360; RRM; 1.
SMART; SM00360; RRM; 1.
SMART; SM00547; Znf_RBZ; 1.
PROSITE; PS50102; RRW; 1.
PROSITE; PS50199; ZF_RANBP2_1; 1.
PROSITE; PS50199; ZF_RANBP2_2; 1.
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RESEQUENCE FROM N.A.

22 STRAIN-C57BL/6J; TISSUE-Head;
23 STRAIN-C57BL/6J; TISSUE-Head;
24 Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
25 Adachi J., Aizawa K., Akahira S., Fukuda S., Fukunishi Y., Furuno M.,
26 Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
27 Arakawa T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
28 Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
29 Arakawa T., Miyazaki A., Nishi K., Nomura K., Nurihara C.,
20 Akawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
20 Akazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
20 Aozaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
20 Aozaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai T.,
21 A. Okazaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
22 Arakawa T., Tayami M., Tagawa A., Takahashi F., Tanaka T.,
23 Arakawa T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
24 Auxamateu M., Hayashizaki Y.,
25 Auxamateu M., Hayashizaki Y.,
26 Auxamateu M., Hayashizaki Y.,
27 Auxamateu M., Hayashizaki Y.,
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MEDLINB=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itch M., Alzawa K., Nagaoka S., Sasaki N., Carninci P.,
Shibata K., Itch M., Alzawa K., Kitsunai T., Tashiro H., Itch M.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itch M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
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GRGGPGGMRGGRGGLMDRGGPGGMFRGGRGGDRGGFRGGRGMDRGGFGGGRRGGPGGPPG
                                                                                                                                                                                                                     GSRGNPSGGGNVQHRAGDWQCPNPGCGNQNFAWRTECNQCKAPKPEGFLPPPFPPPGGDR
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Pred. No. 3.1e
4; Mismatches
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3.1e-73;
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X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X A Klausner R.D., Collins F.S., Wagner L.H., Schaefer C.F., Bhat N.K.,

X Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

X Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

X Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

X Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

X Hopkins R.F., Jordan H., Moore T., Max S.I., Casavant T.L., Scheetz T.E.,

X Hopkins R.F., Jordan H., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

X Hopkins R.F., Joquellan D.K., Toshiyuki S., Carninci P., Prange C.,

X Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

X Brownstein M.J., Wodin T.B., Toshiyuki S., Carninci P., Prange C.,

X Brownstein M.J., Mockernan K.J., Malek J.A., Gunarathe P.H.,

X Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

X Hilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

X Hilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

X Halley J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

X Hilalon D.K., Touchman J.W., Green B.D., Dickson M.C.,

X Hold R.J., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

X Honen S. J. Marra M.A.
                                                                        Query Match
Best Local S
Matches 395
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Q7SZR6;
Q1-CCT-2003 (TrEMBLrel. 25, Created)
01-CCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Wu:fc04c01 protein (Fragment).
QRENAmesewi:fc04c01;
QRENAmesewi:fc04c01;
QRENAmesewi:fc04c01;
                                                                                                                                                                    PROSITE;
NON TER
SEQUENCE
                                                                                                                                                                                                           Pfam; PF00076; RRM, 1; 1.

Pfam; PF00061; zf-RanB; 1.

SMART; SM00360; RRM; 1.

SMART; SM00547; ZnF RBZ; 1.

PROSITE; PS00126; RRM; 1.

PROSITE; PS00216; SUGAR THANSPORT 1; UNKNOWN 1.

PROSITE; PS0158; ZF RANBP2 1; 1.

PROSITE; PS50199; ZF_RANBP2 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jones S.J., Marra M.A.;
"Generation and initial analysis
and mouse cDNA sequences.";
proc. Natl. Acad. Sci. U.S.A. 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brachydanio rerio (Zebrafish)
Bukaryota; Metazoa; Chordata;
Actinopterygii, Neopterygii; T
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R
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BC056281; AAH56281.1; -.
Q9Y5S9; 1P27.
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1 MAS-TDYSTYSQAAAQQGYSAYTAQPTQ-GYAQ-TTQAYG-QQSYGTYGQPTDVSYTQAQ
                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                 IPR000504; RNA_rec_mot.
IPR005829; Sug_transporter.
IPR001876; Znf_RanGDP.
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                                                                          Conservative
                                                                                                                                                                      AA;
                                                                                                                                                                      64517 MW;
                                                                                                51.3%;
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                                                              Pred. No. 1.je
7; Mismatches
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; Craniata; Vertebrata; Euteleostomi;
Teleostei; Ostariophysi; Cypriniformes;
                                                                                              Score 1865; DB 2;
Pred. No. 1.3e-72;
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                                                                          117;
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ID Q9
AC Q9
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Q9BWA2
Q9BWA2;
01-JUN-2001
01-JUN-2001
01-MAR-2003
MEDLINE-22380257; PubMed-12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyaki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                           EWSR1 protein
                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             592
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Primates;
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Last annotation update)
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SEQUENCE FROM N.A.

STRAIN-AB; TISSUE=Whole body;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feligold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.,

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Hopkins R.F., Jordan H.,

Hopkins R.F., Jordan H., Moore T., Max S.I.,

Hopkins R.F., Jordan H., Moore T., Max S.I.,

Hopkins R.F., Jordan H., Moore T.,

Hopkins R.F., Jordan H., Moore T., Max S.I.,

Hopki
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Q803E3; TremBLrel. 24,
01-JUN-2003 (TremBLrel. 24,
01-JUN-2004 (TremBLrel. 26,
                                                                                                                                                                                                                                                                                                      Zgc:55864 protein.
Name=fusl; Synonyms=zgc:55864;
Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniform
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases EMBL; BC000527; AAH00527.1; -. SEQUENCE 354 AA; 37620 MW; AE4B8FCDF458390B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
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"Generation and initial analysis of more than 15,000 and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QPAYPAYGQQPAATAPTRPQDGNKPTETSQPQSSTGGYNQPSLGYGQSNYSYPQVPGSYP
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Pred. No. 5e-6
0; Mismatches
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EMBL; BC044518; AAH44518.1; -...
ZFIN; ZDB-GRNE-030131-1600; fuel.
InterPro; IPR000504; RNA_rec_mot.
InterPro; IPR001876; Znf_RanGDP.
Pfam; PF00076; RRM_1; 1.
Pfam; PF00641; zf-RanBP; 1.
SMART; SM00360; RRM; 1.
SMART; SM003647; Znf_RBZ; 1.
SMART; SM00547; Znf_RBZ; 1.
PROSITE; PS50102; RRM; 1.
PROSITE; PS50199; ZF_RANBP2_1; 1.
PROSITE; PS50199; ZF_RANBP2_2; 1.
SEQUENCE 578 AA; 60625 MW; E950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Buffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S. Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jones S.J., Marra M.A.; "Generation and initial analysis
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              GNVQHRAGDWQCPNPGCGNQNFAWRTECNQCKAPKPEGF-LPPFPFPPPGGDRGRGGPGGM
                                                            GGLPPREGRGMPPPLRGGPGGPGGPGGPMGRMGGRGGDRGGFPPR-GPRGSRGNPSG--G
                                                                                                PMIHIYLDKETGKPKGDATVSYEDPPTAKAAVEWFDGKDFQGSKLKVSLARKKPPMNSMR
                                                                                                                                                YSQ--GGVSGGYPGSQRG----GYQDGGRDGYDRGGPR--GRGMGRGGMGIAGDRGGFNK
                                                                                                                                                                                                                                                     PSAGAYAQQQYGSTYGQAAATAAAAPAAYGTP-QPGAYTQPAQSYGASSYTGSTA-APAA
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                                                                                                                                                                                                                                                                              -QQSSYG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Whole body;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43.5%; Score 1579; Di
50.1%; Pred. No. 2.1e-
tive 65; Mismatches
                                                                                                                                                                                                                                                                            -QQPPTSYPPQTGSYSQAPSQYSQQSSYGQQSSFRQDHPSSMGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E959AACAD7004CD8 CRC64;
                                               GGPGMDRGGMMGRGGERGGFPPRGGPRGGMGWNGGPQP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; DB 2;
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RESULT 15
Q6NWA7
ID Q6NWA7
ID Q6NWA7
DT 05-JT
DT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           XX MEDILINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
XX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
XX Klausner R.D., Collins F.S., Magner L., Shenmen C.M., Schuler G.D.,
XX Klausner R.D., Collins F.S., Magner L., Shenmen C.M., Schuler G.D.,
XX Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
XX Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
XX Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
XX Altschenko L., Marusinia K., Farmer A.A., Rublin G.M., Hong L.,
XX Brapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
XX Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
XX Brans S.S., Loquellano N.A., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
XX Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratte P.H.,
XX Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratte P.H.,
XX Bosak S.A., McCay N., Sodergren E.J., Lu X., Gibbs R.A.,
XX Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
XX Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
XX Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
XX Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
XX Whiting M., Stalska U., Smallus D.E., Schnerch A., Schein J.E.,
XX Cone G. T. M. T., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
XX Cone G. T. M. T., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
                                                                                                                 Query Match
Best Local S
Matches 340
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                          PROSITE; PS50102; RRW; 1.

PROSITE; PS601358; ZF RANBP2 1;
PROSITE; PS60199; ZF RANBP2 2;
NON TER 1
SEQUENCE 575 AA; 60365 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000504; RNA rec mot.
InterPro; IPR001876; Znf RanGDP.
Pfam; PF000076; RRM 1; 1.
Pfam; PF006041; zf RanBP; 1.
SMART; SM00360; RRM; 1.
SMART; SM00547; Znf RBZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases EMBL; BC067661; AAH67661.1; - ZFIN; ZDB-GENE-030131-1600; fusl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation updat
Wu:fb/5g09 protein (Fragment).
Name_fusl; Synonyms=wu:fb/5g09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mouse cDNA sequences.";
c. Natl. Acad. Sci. U.S.A; 99:16899-16903(2002)
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                                                                                                                 340;
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TDYSTYSQAAAQQGYSAYTAQPTQGYAQTT-QAYGQQSYGTYGQPT---DVSYTQAQTTA 59
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                                                                                                          43.1%; Score 1566; DB 2; Length 575;
49.9%; Pred. No. 7.7e-60;
tive 65; Mismatches 141; Indels 136;
                                                                                                                                                                                                                                                                 A1650072377A7629 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          578
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                         GRGGPGKMDKGEHRQERRDRPY
                                                                                                         QKRAGDWECPNAGCGNONFSWRMECNOCKAPKPEGLGTSPPF-SPGGERGR--
                                                                                                                         OHRAGDWQCDNPGCGNQNFAWRTECNQCKAPKPEGF-LPPPFPPPPGGDRGRGGPGGMRGG
                                                                                                                                                                                PPREGRGMPPPLRGGPGGPGGPGGPMGRMGGRGGDRGGFPPR-GPRGSRGNPSG--GGNV
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                                                                                                                                                                                                                                                                          --GGVSGGYPGSQRG----GYQDGGRDGYDRGGPR--GRGMGRGGMGIAGDRGGFNKPGG
                                                                                                                                                                                                                                                                                                                                                                                    SAYGQGQPPQQHQQGPPAAYPPQ-GSSSYAQTQYGQQSA---PQNDYQQNPYNS---YSQ
                                                                                                                                                                                                                                                                                                                                                                                                               SSYG------QOPPTSYPPQTGSYSQAPSQYSQQSSSYGQQSSFRQDHPSSMGVYGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -TYGQTAYATSYGQ------PPTGYTTPTAPQAYSQPVQGYGTGAYDTTTATVTTTQAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TNYSSYNQAGAQQSYGSYTAPPAQTYGQTAQQGYTQQDYSSYAQPAAAPEATYSQAAPSA 60
                                                    RG--MDRGGPGGM-RGGWGGDRGGFRGKGGMDRGGFRGGSRGGP-----PMDRGRR
                                                                    RGGIMDRGGPGGMFRGGRGGDRGGFRGGRGMDRGGFGGGRRGGPPGPPMEQMGGRRG
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GMGPPGKMEMRDHRQERRERPY
                                                                                                                                                                 -GGPGMDRGGMMGRGGERGGFPPRGGPRGGMGWNGGPQPGNV
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Search completed: February 18, 2005, 15:12:07 Job time : 181 secs

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Result
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-MODEL-frame+ p2n.model -DEV=xlp
-MODEL-frame+ p2n.model -DEV=xlp
-MODEL-frame+ p2n.model -DEV=xlp
-Q-/Ggn2_1/USPTO_Spool_p/US10791017/runat_17022005_125807_22074/app_query.fasta_1.1358
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LGOPCL=0 -LGOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER-US10791017_@CGN 1 1_7357_@runat_17022005_125807_22074 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORE—100 -THREADS-1 -ZGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-DEV_TIMEOUT=120 -MARN_TIMEOUT=30 -THREADS-1 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELOP=6 -DELEXT=7
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Perfect score:
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Maximum DB
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                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                 Score
     3633
3633
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seq length: 2000000000
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Ygapop 10.0,
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Copyright (c) 1993 - 2005
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BT007796 Synthetic
BC004817 Homo sapi
A36460 Sequence 1
AR080100 Sequence
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ALIGNMENTS

JOURNAL REFERENCE AUTHORS ACCESSION VERSION KEYWORDS SOURCE REFERENCE AUTHORS LOCUS DEFINITION COMMENT TITLE JOURNAL TITLE ORGANISM 2 (bases 1 to 1971)

Kalnine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S., Koundinya,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y., Phelan,M. and Farmer,A.

Direct Submission

Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Meadow Circle, Palo Alto, CA 94303, USA

This CDS clone is a part of a collection of human full length expression clones generated by BD Biosciences Clontech and the Harvard Institute of Proteomics. Each CDS has been cloned in two other sequences; artificial sequences.

1 (bases 1 to 1971)

Kalnine, N., Chen, X., Rolfs, A., Halleck, A., Hines, L., Eisenstein, S., Koundinya, M., Raphael, J., Moreira, D., Kelley, T., LaBaer, J., Lin, Y., Phelan, M. and Farmer, A.

Cloning of human full-length CDSs in BD Creator (TM) System Donor FLI CDNA.
synthetic construct
synthetic construct Unpublished mRNA, partial cds. BT007796 BT007796 1 Synthetic construct Homo vector BT007796.1 GI:30584430 1971 bp mRNA linear SYN 13 sapiens Ewing sarcoma breakpoint SYN 13-MAY-2003

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                                                                                                       ThrAlaProGlnAlaTyrSerGlnProValGlnGlyTyrGlyThrGlyAlaTyrAspThr
                                                                                                                                                                                                                                                              TyrThrAlaGlnProThrGlnGlyTyrAlaGlnThrThrGlnAlaTyrGlyGlnGlnSer
                                                                                                                                                                                                                                                                                                                      MetAlaSerThrAspTyrSerThrTyrSerGlnAlaAlaAlaGlnGlnGlyTyrSerAla
 GlnProAlaTyrProAlaTyrGlyGlnGlnProAlaAlaThrAlaProThrArgProGln
                                             ThrThrAlaThrValThrThrThrGlnAlaSerTyrAlaAlaGlnSerAlaTyrGlyThr
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                                                                                                                                               TATGGGCAGACCGCCTATGCAACTTCTTATGGACAGCCTCCCACTGGTTATACTACTCCA
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/mol_type="mRNA"
/mol_type="mRNA"
/db xrefs"ttaxon:32630"
/clone="GH00297L1.0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LMEQMGGRRGGRGGPGKMDKGEHRQERRDRPYL"
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/protein_id="AAP36468.1
/db_xref="GI:30584431"
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note="Vector: pDNR-Dual"
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                                                           ArgGluGlyArgGlyMetProProProCeuArgGlyGlyProGlyGlyProGlyGlyPro
                                                                                                                    LysValSerLeuAlaArqLysLysProProMetAsnSerMetArqGlyGlyLeuProPro
                                                                                                                                                               CCCACTGCCAAGGCTGCCGTGGAATGGTTTGATGGGAAAGATTTTCAAGGGAGCAAACTT
                                                                                                                                                                               ProThrAlaLysAlaAlaValGluTrpPheAspGlyLysAspPheGlnGlySerLysLeu
                                                                                                                                                                                                                       TACCTGGACAAGGAAACAGGAAAGCCCAAAGGCGATGCCACAGTGTCCTATGAAGACCCA
                                                                                                                                                                                                                                          TyrLeuAspLysGluThrGlyLysProLysGlyAspAlaThrValSerTyrGluAspPro
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                                                                                                                                    Strauberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.K.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Scheetz, T.E., Brownstein, M.J., Ugdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

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2182 bp mRNA linear PRI 29-JUN-2004
Homo sapiens Ewing sarcoma breakpoint region 1, transcript variant
EWS, mRNA (cDNA clone MGC:5432 IMAGE:3449145), complete cds.
     Direct Submission
Submitted (21-MAR-2001) National
                                                                Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                        (bases 1 to 2182)
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     Institutes of Health, Mammalian
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Best Local Similarity:
Query Match:
                                                                                        US-10-791-017A-2 (1-656) x BC004817
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1 MetAlaSerThrAspTyrSerThrTyrSerGlnAlaAlaAlaGlnGlnGlyTyrSerAla 20
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Length:
Matches:
Conservative:
Mismatches:
Indels:

(1-2182)

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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 3 Row: 1 Column: 6 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
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Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590
USA
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Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny,
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Tissue Procurement: ATCC
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Contact: MGC help desk
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2 ATGCCOTCOLCGGATTACAGTACCTATAGCCAACCGCACCAGCCACCAGCCATCCAT
99 181 PhetyredinyrallyallyallyalverAnnilyaArghthciydilprownetileHisile 100 1100 TTPANGAGTTANGAGTTANGAGTANGAGAACACCARGTTCGARTCCART (2139 0) 201 TYPIANGAGTANGAGAACACCARGTTCGARTCCART (2139 0) 202 TACCCGARTCCARGTTCGARGTTCGARTCCARGTTCGARTCCARGTTCGARTCCARGTTCGARTCCARGTTCGARTCCARGTTCGARTCCARGTTCGARTCCARGTTCGARTCCARGTTCGARTCCARGTTCGARTCCARGTTCGARTCCARGTTCGARTCCARGTTCGARTCCARGTTCGARTCGAR

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241 ProProGlnThrGlySerTyrSerGlnAlaProSerGlnTyrSerGlnGlnSerSerSer 260	221 GlyGlnGlnSerSerTyrGlyGlnGlnSerSerTyrGlyGlnGlnProProThrSerTyr 240 	201 ThrSerTyrAspGlnSerSerTyrSerGlnGlnAsnThrTyrGlyGlnProSerSerTyr 220 	181 MetGlnProValThrAlaProProSerTyrProProThrSerTyrSerSerThrGlnPro 200 	161 ProSerLeuGlyTyrGlyGlnSerAenTyrSerTyrProGlnValProGlySerTyrPro 180 	141 AspGlyAsnLysProThrGluThrSerGlnProGlnSerSerThrGlyGlyTyrAsnGln 160 	121 GlnProAlaTyrProAlaTyrGlyGlnGlnProAlaAlaThrAlaProThrArgProGln 140	101 ThrThrAlaThrValThrThrGlnAlaSerTyrAlaAlaGlnSerAlaTyrGlyThr 120	81 ThralaProGlnAlaTyrSerGlnProValGlnGlyTyrGlyThrGlyAlaTyrAspThr 100 	61 TyrGlyGlnThrAlaTyrAlaThrSerTyrGlyGlnEroProThrGlyTyrThrThrEro 80	41 TyrGlyThrTyrGlyGlnProThrAspValSerTyrThrGlnAlaGlnThrThrAlaThr 60	21 TyrThrAlaGlnProThrGlnGlyTyrAlaGlnThrThrGlnAlaTyrGlyGlnGlnSer 40	1 MetAlaSerThrAspTyrSerThrTyrSerGlnAlaAlaAlaGlnGlnGlyTyrSerAla 20 	6 Gaps: 6) x A36460 (1-2371)	6.22e-77 3633.00 milarity: 100.00% L Similarity: 100.00% ch: 100.00%	Scores:	/organiama"Homo sapiens" /organiama"Homo sapiens" /mol_type="unassigned DNA" /db xref="taxon:9606" /dev_stage="FOETUS"		DEVELOPMENT OF CANCEROUS TUMORS L Patent: WO 9323549-A 1 25-NOV-1993; CENTRE NAT RECH SCIENT (FR)
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601 GLYGIYATGIJYMEKABATGGIYGIYYENEGIYGIYAIYATGATGGIYGIYETGGIYGIY 														321 ArgGlyGlyMetGlySerAlaGlyGluArgGlyGlyPheAsnLysProOlyGlyProMet		281 Glusergiyeiyehesergiyerogiygilaanargsermetsergiyeroaspasnarg	805 TACGGGCAGCAGAGTTCATTCCGACAGGACCACCCCAGTAGCATGGGTGTTTATGGGCAG	745 CCACCCCAAACTGGATCCTACAGCCAAGCTCCAAGTCAATATAGCCAACAGAGCAGCAGC 261 TyrGlyGlnGlnSerSerPheArgGlnAspHisProSerSerMetGlyValTyrGlyGln

Db 205 TATGGGCAGACCGCTATGCAACTTCTTATGGACAGCCTCCCACTGGTTATACTACTACTACTACTACTACTACTACTACTACTACT	25 Arddedrichedarthachdracharhadechadeddeddaddaddaddaddaddaddaddaddaddaddad	ignment Scores:	Aur Plo Nuc dev reg Pat	AR080100 2371 bp DNA lin Sequence 1 from patent US 5968734. AR080100 AR080100.1 GI:10006835 Unknown. Unknown. Unclassified. 1 (bases 1 to 2371)	Qy 621 ProProGlyProLeumetGluGlnMetGlyGlyArgArgGlyGlyArgGlyGlyProGly 640
441 LysVallSerLeuAlaArgLysElysBroProMetAsnSerMetArgGlyGlyLeuProPro 1345 AAAGTCTCCCTTGCTCGAAGAAGCCTCCAATGAACAGTATGCGGGGTGGTCTGCCACCC 461 ArgGluGlyArgGlyMetProProProLeuArgGlyGlyProGlyGlyProGlyGlyPro 1405 CGTGAGGGCAGGCATGCCACCCACTCCGTGGAGGTCCAGGAGGCCCAGGAGGTCCT 481 GlyGlyProMetGlyArgMetGlyArgGlyArgGlyAspArgGlyGlyPheProProArg	381 PheLysGlnCysGlyValValLysMetAsnLysArgThrGlyGlnProMetIleHisIle	321 ArgGlyGlyMetGlySerAlaGlyGluArgGlyPheAsnLysProGlyGlyProMet 3	Db 745 CCACCCAAACTGGATCCTACAGCCAAGCTCCAAGTCAATATAGCCCAACAGAGCAGC 804 Qy 261 TyrGlyGlnGlnSerSerPheArgGlnAepHisDroSerSerMetGlyValTyrGlyGln 280	201 ThrserTyrAspGlnSerSerTyrSerGlnGlnAsnThrTyrGlyGlnProSerSerTyr 2	Db 445 GATGGAAACAAGCCCACTGAGACTAGTCAACCTCAATCTAGCACAGGGGGTTACAACCAG 504 Qy 161 ProSerLeuGlyTyrGlyGlnSerAsnTyrSerTyrProGlnValProGlySerTyrPro 180

/or /db /db /db /oo /co /co /co /co /co /co /co /co /co	RESULT 5 CQ867364 CQ867364 CQ867364 CQ867364 VERSION CQ867364 VERSION CQ867364.1 GI:51997589 SOURCE ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; REFERENCE AUTHORS TITLE JOURNAL FEATURES SOURCE SOURCE JOURNAL Schering Aktlengesellschaft (DE) FEATURES SOURCE LOSSION CQ867364.1 GI:51997589 Eutharyota; Metazoa; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE JOURNAL Schering Aktlengesellschaft (DE) FEATURES SCHERING LOSSION CQ867364.1 GI:51997589 Eutheryota; Craniata; Vertebrata; Euteleostomi; REFERENCE LOSSION CQ867364.1 GI:51997589 Eutheryota; Country Craniata; Vertebrata; Euteleostomi; REFERENCE LOSSION CQ867364.1 GI:51997589 Eutheryota; Country Craniata; Vertebrata; Euteleostomi; REFERENCE LOSSION CQ867364.1 GI:51997589 Eutheryota; Country Craniata; Vertebrata; Euteleostomi; REFERENCE LOSSION CQ867364.1 GI:51997589 Eutheryota; Craniata; Vertebrata; Eutheryota; Craniat	Oy 521 AspTrpGlnCysProAsnProGlyCysGlyAsnGlnAsnPheAlaTrpArgThrGluCys GACTGGCAGTGTCCAATCCGGGTTGTGAAAACCAGAACTTCGCCTGGAGAACAGAGAGTGC 1644 Oy 541 AsnGlnCysLysAlaProLysProGluGlyPheLeuProProProProProProProGly GACCAGTGTAAGGCCCCAAAGCCTGAAGGCTTCCTCCGCCCAACCCTTTCCGCCCCGGT 1704 Oy 561 GlyAspArgGlyArgGlyGlyProGlyGlyMetArgGlyGlyArgGlyGlyArgGlyGlyLeuMetAsp Db 1705 GGTGATCGTGGCAGAGGTGGCCCTGGTGGAGAAAGAGAGGTGGCCTCATGAT 1764 Oy 581 ArgGlyGlyProGlyGlyMetPheArgGlyGlyArgGlyGlyAspArgGlyGlyPheArg GO 601 GlyGlyArgGlyMetPheArgGlyGlyArgGlyGlyAspArgGlyGlyProGlyGly GO 601 GlyGlyArgGlyMetAspArgGlyGlyPheGlyGlyArgArgGlyGlyProGlyGly GO 601 GlyGlyArgGlyMetAspArgGlyGlyPheGlyGlyArgArgGlyGlyProGlyGly GO 601 GlyGlyArgGlyMetAspArgGlyGlyPheGlyGlyArgArgGlyGlyProGlyGly GO 601 GlyGlyArgGlyMetAspArgGlyGlyPheGlyGlyArgArgGlyGlyProGlyGly GO 601 GlyGlyArgGlyProLeuMetGluGlmMetGlyGlyArgArgGlyGlyArgGlyGlyProGlyGly GO 621 ProProGlyProLeuMetGluGlmMetGlyGlyArgArgGlyGlyArgGlyGlyProGlyGly GO 621 ProProGlyProLeuMetGluGlmMetGlyGlyArgArgGlyGlyArgGlyGlyProGlyGly GO 641 LysMetAspLysGlyGluHisArgGlnGluArgArgAspArgBroTyr G56
	121 GlnProAlaTyrProAlaTyrGlyGlnGlnProAlaAlaThrAlaProThrArgProGln	Best Local Similarity: 100.00% Mismatches: 0 Query Match: 100.00% Indels: 0 BB: 0 Opery Match: 6 Gaps: 0 Indels: 0 Opery Match: 6 Gaps: 0 Opery Match: 6 Gaps: 0 Opery Match: 6 Gaps: 0 Indels: 0 Opery Match: 6 Gaps: 0 Indels: 0 Opery Match: 6 Gaps: 0 Indels: 0

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Sequence 37:
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 Homo
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                                                                                                          LysMetAspLysGlyGluHisArgGlnGluArgArgAspArgProTyr
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Butheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alvares,C., Horne,D., Peres-da-Silva,S. and Gene expression profiles in liver cancer Patent: WO 0229103-A 3772 11-APR-2002; GENE LOGIC INC (US)
                                                                         MetGlnProValThrAlaProProSerTyrProProThrSerTyrSerSerThrGlnPro
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                                    GlyGlnGlnSerSerTyrGlyGlnGlnSerSerTyrGlyGlnGlnProProThrSerTyr
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X66899
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translocation in human tumours
Nature 359 (6391), 162-165 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Delattre,O., Zucman,J., Plougastel,B., Desmaze,C., Melot,T., Peter,M., Kovar,H., Joubert,I., de Jong,P., Rouleau,G., Aurias,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fusion with an ETS DNA-binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GI:547565
                                                                                                                                                                                                                                                                                                                                                                                           /gene="EWS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /chromosome="22q12"
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ACCITICATION OF THE PROPERTY O	luThrSerGlnProGlnSe	Oy 101 ThrThrAlaThrValThrThrGlnAlaSerTyrAlaAlaGlnSerAlaTyrGlyThr 120	Qy 61 TyrGlyGlnThrAlaTyrAlaThrSerTyrGlyGlnProProThrGlyTyrThrThrPro 80	aGlnProThrGlnGlyTyrAlaGlnThrThrGlnAlaTyrGlyGlnGlr 	1 MetAlaSerThrAspTyrSerT	giment scores: d. No.: 6.25e-77 re: 3633.00 cent Similarity: 100.00% t Local Similarity: 100.00% ry Match: 9 10-701-017A-2 (1-556) x HSPWS	yA_sign yA_sign yA_site
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561 GlyAspargGlyArgGlyProGlyGlyMetArgGlyGlyArgGlyGlyLeuMetAsp 580		1424 CGTGAGGCAGAGGCATCCACCACTCCGTGGAGGTCCAGGAGGCCCAGGAGGTCCT 1483 481 GlyGlyProMetGlyArgMetGlyGlyArgGlyGlyAspArgGlyGlyPheProProArg 500	1304 CCCACTGCCAAGGCTGCCGTGAATGGTTTGATGGGAAAGATTTTCAAGGGAGCAAACTT 1363 441 LysValSerLeuAlaArgLysLysProProMetAsnSerMetArgGlyGlyLeuProPro 460	1184 TTTAAGCAGTGTGGGGTTGTTAAGATGAACAAGAGAACTGGGCAACCCATGATCCACATC 1243 401 TyrLeuAspLysGluThrGlyLysProLysGlyAspAlaThrValSerTyrGluAspPro 420	361 SerAlaileTyrValGlnGlyLeuAsnAbpSerValThrLeuAspAspLeuAlaAspPhe 380	321 ArgGlyGlyMetGlySerAlaGlyGluArgGlyGlyPheAsnLysProGlyGlyProMet 340	

RESULT 8 BC072442

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LOCUS DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE

AUTHORS

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Strausberg, L., Feligold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buctow, K.H., Schaefer, C.F., Bhat, N.K.,

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Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahay, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Fahay, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Bouffard, G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Schmerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                        CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc.mgc@nhgri.nih.gov
Akhter,N., Ayele,K. Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
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Young,A., Zhang,L.-H. and Green,B.D.
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Clone distribution: MGC clone distribution information can be foun through the I.M.A.G.E. Consortium/LINI at: http://image.llnl.gov Series: IRAK Plate: 174 Row: g Column: 18
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4885224.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (01-JUN-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BC072442 2164 bp mRNA linear PRI 30-JU
Homo sapiens Ewing sarcoma breakpoint region 1, transcript va
EWS, mRNA (cDNA clone MGC:87992 IMAGE:6047805), complete cds.
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BC072442.1 GI:48734726
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Best Local Similarity:
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     GlnProAlaTyrProAlaTyrGlyGlnGlnProAlaAlaThrAlaProThrArgProGln
                                                                                                                                                                                                                         ThrAlaProGlnAlaTyrSerGlnProValGlnGlyTyrGlyThrGlyAlaTyrAspThr
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                                                                                                                                       ThrThrAlaThrValThrThrGlnAlaSerTyrAlaAlaGlnSerAlaTyrGlyThr
                                                                                                                                                                                           ACTGCCCCCAGGCATACAGCCAGCCTGTCCAGGGGTATGGCACTGGTGCTTATGATACC
                                                                                                                                                                                                                                                                                                  TATGGGCAGACCGCCTATGCAACTTCTTATGGACAGCCTCCCACTGGTTATACTACTCCA
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99.85%
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PUBMED REFERENCE AUTHORS TITLE JOURNAL

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Submitted (24-MAY-2004) Sanger Institute, Hinxton, Cambridgeshire, CB10 ISA, UK. E-mail enquiries: c22g@sanger.ac.uk Manuscript Sanger Institute name: pGEM.EWSR1 Homo sapiens cDNA sequence. This sequence was generated as part of The Wellcome Trust Sanger Institute program to isolate cDNA clones representing the full length open reading frame of well annotated protein coding genes on human chromosome 22. For more information. see http://www.sanger.ac.uk/HGP/Chr22/.
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CR456490.1 GI:47678510
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(CDNA clone C22ORF:pGEM.EWSR1).
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; E

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae;

1 (bases 1 to 2189)

1 (bases 1 to 2189)

Collins, J.E., Wright, C.L., Edwards, C.A., Davis, M.P.,

Collins, J.E., Goward, M.E., Aguado, B., Mallya, M., Mokrab,

Huckle, E.J., Beare, D.M. and Dunham, I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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S Ś ঠ S 음 성 뭥 밁 문 밁 8 밁 ઇ 밁 밁 ঠ 밁 S 문 ई 밁 Ş 밁 Percent Similarity:
Best Local Similarity:
Query Match:
DB: र् S Alignment US-10-791-017A-2 (1-656) x CR456490 Pred. No.: 241 694 221 634 201 574 181 514 161 454 141 394 121 334 101 274 214 154 81 61 41 94 21 34 MetGlnProValThrAlaProProSerTyrProProThrSerTyrSerSerThrGlnPro ProSerLeuGlyTyrGlyGlnSerAsnTyrSerTyrProGlnValProGlySerTyrPro ThrAlaProGlnAlaTyrSerGlnProValGlnGlyTyrGlyThrGlyAlaTyrAspThr TATGGGCAGACCGCCTATGCAACTTCTTATGGACAGCCTCCCACTGGTTATACTACTCCA TyrGlyGlnThrAlaTyrAlaThrSerTyrGlyGlnProProThrGlyTyrThrThrPro TyrThrAlaGlnProThrGlnGlyTyrAlaGlnThrThrGlnAlaTyrGlyGlnGlnSer MetAlaSerThrAspTyrSerThrTyrSerGlnAlaAlaGlnGlnGlyTyrSerAla GGACAGCAGAGTAGCTATGGTCAACAAAGCAGCTATGGGCAGCAGCCT GlyGlnGlnSerSerTyrGlyGlnGlnSerSerTyrGlyGlnGlnProProThrSerTyr CCCAGCCTAGGATATGGACAGAGTAACTACAGTTATCCCCAGGTACCTGGGAGCTACCCC ProProGlnThrGlySerTyrSerGlnAlaProSerGlnTyrSerGlnGlnSerSerSer 1.29e-76 3618.50 99.85% 99.85% 99.60% (1-2189)Length:
Matches:
Conservative:
Mismatches:
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Gaps: 753 693 220 573 180 513 160 453 140 393 120 333 100 273 633 80 213 60 153 40 ٠ 5 밁 Ś 밁 S 片 S 밁 8 밁 S 밁 ð 밁 5 밁 Ś 맑 ঠ Ś 밁 밁 5 片 밁 S 밁 Ś 밁 S S 밁 S 문 S 문 1711 1531 1471 1411 1351 1291 1231 1171 1051 501 481 461 421 401 381 321 934 301 281 754 AspTrpGlnCysProAsnProGlyCysGlyAsnGlnAsnPheAlaTrpArgThrGluCys GlyAspArgGlyArgGlyGlyProGlyGlyMetArgGlyGlyArgGlyGlyLeuMetAsp GlyGlyProMetGlyArgMetGlyGlyArgGlyGlyAsgArgGlyGlyPheProProArg ArgGlyGlyProGlyGlyMetPheArgGlyGlyArgGlyGlyAspArgGlyGlyPheArg GGTGATCGTGGCAGAGGTGGCCCTGGTGGCATGCGGGAGGAAGAGGTGGCCTCATGGAT AACCAGTGTAAGGCCCCAAAGCCTGAAGGCTTCCTCCCGCCACCCTTTCCGCCCCCGGGT AsnGlnCysLysAlaProLysProGluGlyPheLeuProProProPheProProProGly ArgGluGlyArgGlyMetProProProLeuArgGlyGlyProGlyGlyProGlyGlyProCleuArgGluGlyProGlyGlyProGlyGlyProCleuArgGluGlyGlyProCleuArgGluGlyGlyProCleuArgGluGlyProGlyGlyProCleuArgGluGlyProGlyGlyProCleuArgGluGlyProGlyGlyProCleuArgGluGlyProGlyGlyProGlyGlyProCleuArgGluGlyProGlyGlyGlyProGlyGlyGlyProGlyGlyGlyProGlyGlyGlyProGlyGlyGlyProGlyGlyGlyProGlyGlyGlyProGlyGlyGlyProGlyGlyGlyProGlyGlyGlyProGlyGlyProGlyGlyGlyProGlyGlyGlyProGlyGlyGlyProGlyGlyGlyProGlyGlyGlyProGlyGlyGlyGlyProGlyGlyGlyGlyFroGlyGlyGlyGlyFroGlyGlyGlyGlyGlyFroGlyGlyGlyGlyFroGlyGlyGlyGlyGlyGlyFroGlyGlyGlyGlyFroGlyGlyGlyGlyFroGlyGlyGlyGlyFroGlyGlyGlyGlyFroGlyGlyGlyFroGlyGlyGlyFroGlyGlyGlyFroGlyGlyGlyFroGlyGlyGlyFroGlyGlyGlyFroGlyGlyGlyFroGlyGlyGlyFroGlyGlyGlyFroGlyGlyGlyFroGlyGlyGlyFroGlyGlyGlyGlyFroGlyGlyGlyGlyFroGlyGlyGlyGlyFroGlyGlyGlyFroGlyGlyGlyFroGlyGlyGlyFroGlyGlyGlyFroGlyGlyGlyFroGlyGlyGlyFroGlyGlyGlyFroGlyGlyGlyFroGlyFroGlyFroGlyGlyFroGlyFroGlyFroGlyGlyFroGlyGlyFroGlyFroGlyGlyFroGlyFroGlyGlyFroGlyFroG CCCACTGCCAAGGCTGCCGTGGAATGGTTTGATGGGAAAGATTTTCAAGGGAGCAAACTT ProThrAlaLysAlaAlaValGluTrpPheAspGlyLysAspPheGlnGlySerLysLeu TyrLeuAspLysGluThrGlyLysProLysGlyAspAlaThrValSerTyrGluAspPro PheLysGlnCysGlyValValLysMetAsnLysArgThrGlyGlnProMetIleHisIle AGTGCAATTTATGTACAAGGATTAAATGACAGTGTGACTCTAGATGATCTGGCAGACTTC SerAlaIleTyrValGlnGlyLeuAsnAspSerValThrLeuAspAspLeuAlaAspPhe GATGAAGGACCAGATCTTGATCTAGGCCCACCTGTAGATCCAGATGAAGACTCTGACAAC AspGluGlyProAspLeuAspLeuGlyProProValAspProAspGluAspSerAspAsn ArgGlyGlyMetGlySerAlaGlyGluArgGlyGlyPheAsnLysProGlyGlyProMet GluSerGlyGlyPheSerGlyProGlyGluAsnArgSerMetSerGlyProAspAsnArg 1770 1710 1650 1530 480 440 1290 1170 1830 600 580 1590 1470 1410 460 1350 1230 400 1110 1050 540 520 420 380 360 340 300 993 933 873 813

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AUTHORS
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsleh, F.,
Diatchenko, L., Warusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Uddin, T.B., Toshiyuki, S.,
Garninci, P., Prange, C., Raha, S.S., Loquellano, M.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
12477932
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                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genom
Clone distribution: MGC clone distribution information can be four through the I.M.A.G.E. Consortium/LIML at: http://image.llnl.gov Series: IRAK Plate: 12 Row: p Column: 1
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4885224.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (25-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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                                                                                                                                                                                                                                  Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                         Sequencing Center
Center code: BCM-HGSC
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                         SGGGNVQHRAGDWQCPNPGCGNQNFAWRTECNQCKAPKPEGFLPPPFPPPGGDRGRGG
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                         121
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                                                                                                                                     81 ThrAlaProGlnAlaTyrSerGlnProValGlnGlyTyrGlyThrGlyAlaTyrAspThr
                                                                                                                                                                                                61 TyrGlyGlnThrAlaTyrAlaThrSerTyrGlyGlnProProThrGlyTyrThrThrPro
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                                                                                                                      ACTGCCCCCCAGGCATACAGCCAGCCTGTCCAGGGGTATGGCACTGGTGCTTATGATACC
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            LysMetAspLysGlyGluHisArgGlnGluArgArgAspArgProTyr 656
                                                                                                                                                                                                                                                                                       AspTrpGlnCysProAsnProGlyCysGlyAsnGlnAsnPheAlaTrpArgThrGluCys
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SOURCE ORGANISM RESULT 11 AK056309 LOCUS VERSION KEYWORDS ACCESSION DEFINITION

REFERENCE AUTHORS oligo capping; fis (full insert sequence)
Homo sapiens (human)
Homo sapiens 2189 bp Homo sapiens cDNA FLJ31747 fis, to RNA-BINDING PROTEIN EWS.
AK056309 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. mRNA linear PRI 30-JAN-2004 clone NT2RI2007377, highly similar

Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R., Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Sekine, M., Obayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahari, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M., Sifratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T., Kikawa, E., Omura, Y., Abe, K., Kamahara, K., Katsuta, M., Sato, K., Tanikawa, M., Yamazaki, M., Ninomiya, K., Ishibashi, T., Yamashita, H., Murakawa, K., Pujimori, K., Tanai, H., Kimata, M., Watanabe, M., Hiraoka, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S., Yosida, M., Hotuta, T., Kusano, J., Kanehori, K., Takahashi, Pujii, A., Hara, R., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Imose, N., Musashino, K., Yuuki, H., Oshima, A., Sasaki, N., Aotsuka, S., Yoshikawa, Y., Meunawa, H., Ichihara, T., Shinata, N., Satoh, A., Mizoguchi, H., Takama, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H., Takama, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H., Kawakami, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Satoh, T., Kama, Y., Okamoto, S., Okitani, R., Hikiji, T., Kobatake, N., Nakajawa, M., Basaki, M., Togashi, T., Nomiyama, M., Satoh, T., Morinaga, M., Sasaki, M., Togashi, T., Natanabe, M., Satoh, T., Shirai, Y., Okamoto, S., Okitani, R., Kawakami, T., Nomura, K., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Satoh, T., Natanabe, M., Kawakami, T., Natanabe, M., Sasaski, M., Togashi, T., Natanabe, M., Sasaski, M., Togashita, R., Kawakami, T., Natanabe, M., Kawakami, T.,

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JOURNAL
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US-10-791-017A-2 (1-656) x AK056309 (1-2189)
                                                                     Query Match:
DB:
                                                                                                                            Best Local Similarity:
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CE 3 (bases 1 to 2189)

RS Isogai, T., Otsuki, T. and Sugiyama, T.

Direct Submission

AL Submitted (24-CCT-2001) Takao Isogai, Helix Research Institute,

Genomics Laboratory,:1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of

Economy, Trade and Industry of Japan, cDNA full insert sequencing:

Research Association for Biotechnology (RAB); cDNA library

construction: Helix Research Institute (HRI) (supported by Japan

Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,

HRI, and Biotechnology Center, National Institute of Technology and

Evaluation; clone selection for full insert sequencing: RAB and

HRI.
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TYGQESSYGQOSSYGQQSSYGQDSSTAGAGE
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KONKRYGGPMHHIYLDKETGKKKGDATYSYEDPTAKAAVEMFDGKDFQGSKLKVSLA
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/clone lib="NYT2RI2"
/note="cloning vector: pME18SFL3-mRNA from NT2 neuronal precursor cells treated 2-weeks mitotic inhibitor after 5-weeks retinoic acid (RA) induction.~majorly NT2 neuron"
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GSRGNPSGGGNVQHRAGDWQCPNPGCGNQNFAWRTECNQCKAPKPEGFLPPPPPPGG
DRGRGGPGGMRGGRGGLMDRGGPGGMPRGGRGGDRGGFRGGRGMDRGGFGGGRRGGPG
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/db_xref="GI:16551674"
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/db_xref="taxon:9606"
/clone="NT2RI2007377"
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1 MetAlaSerThrAspTyrSerThrTyrSerGlnAlaAlaAlaGlnGlnGlyTyrSerAla 20

pSerValThrLeu 374	355 AspGluAspSerAspAsnSerAlaIleTyrValGlnGlyLeuAsnAspSe: 	Ş
CCTGTAGATCCA 1	ũ	망
ProValAspPro 354	35 LygProGlyGlyProMetAspGluGlyProAspLeuAspLeuGlyPro	Q
gGlyGlyPheAsn 334	315 GlyGlyArgGlyGlyArgGlyGlyMetGlySerAlaGlyGluArg 	유 성
AGGCATGAGC	TGATCGTGC	문
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GAACCGGAGCATG 921	2 ATGGGTGTTTATGGGCAGGAGTCTGGAGGATTTTCCGGACCAGGAG	B &
nargerMet 2	75	? 5
\spHisProSerSer 274	S5 SerGlnGlnSerSerSerSerTyrGlyGlnGlnSerSerPheArgGlnZ	3 8
CCAAGTCAA	42 CAGCCTCCCACTAGTTACCCACCCCAAACTGGATCCTACAGCCAAGCT	Дb
- 7	35 GlnProProThrSerTyrProProGlnThrGlySerTyrSerGlnAla	Ş
CAGCTATGGGCAG 741	82 GGCAACCGAGCTATGGACAGCAGAGTAGCTATGGTCAACAAAGC	망
serTyrGlyGl	15 GlyGlnProserserTyrGlyGlnGlnSerserTyrGlyGlnGlnSer	Ś
GCAGAACACCTAT 681	622 TATTCCTCTACACAGCCGACTAGTTATGATCAGAGCAGTTACTCTCAGC	망
lnAsnThrTy	95 TyrSerSerThrGlnProThrSerTyrAspGlnSerSerTyrSerG	Ş
CCTCCTACCAGC	562 GTACCTGGGAGCTACCCCATGCAGCCAGTCACTGCACCTCCATCCTAC	Дb
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AGTTATCCCCAG	02 ACAGGGGGTTACAACCAGCCCAGCCTAGGATATGGACAGAGTAACTA	Дb
SerTyrPro	ss ThrolyGlyTyrAenGlnBroSerLeuGlyTyrGlyGlnSerAenTy	ঠ
CTCAATCTAGC	42 GCACCTACAAGACCGCAGGATGGAAACAAGCCCACTGAGACTAGTCAA	뮰
ProGlnSerSe	35 AlaproThrArgProGlnAspGlyAsnLysProThrGluThrSerGln	ş
nProAlaAlaThr 134 CCAGCAGCCACT 441	115 GlnSeralaTyrGlyThrGlnProAlaTyrProAlaTyrGlyGlnGlnP- 	β Q
CTATGCAGC	22 ACTGGTGCTTATGATACCACCACTGCTACAGTCACCACCAGCCAG	Д
\laSerTyrAlaAla 114	95 ThrGlyAlaTyrAspThrThrThrAlaThrValThrThrThrGlnAla	ঠ
ନ୍ଥ=	2 ACAGGITATACTACTCCAACTGCCCCCCAGGCATACAGCCAG	DЬ
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CCACTGTAGAAGGGACCAGT 261	2 TATGGGCAGACCGCCTATGCAACTTCTTATGGACAGCCTC	Дb
74	rGlyGlnThrAlaTyrAlaThrSerTyrGlyGlnProP	ঠ
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Homo sapiens (human)
Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                         CQ730352
Sequence 16286 from Pat
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                                                                                                                    ProTyr
                                                                                                                                                                     AspärgGlyGlyPheArgGlyGlyArgGlyMetAspärgGlyGlyFheGlyGlyGlyArg
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                                                 ValThrThrThrGlnAlaSerTyrAlaAlaGlnSerAlaTyrGlyThrGlnProAlaTyr
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                  SerTyrGlyGlnGlnSerSerTyrGlyGlnGlnProProThrSerTyrProProGlnThr
                                                                                                                    TATGGACAGAGTAACTACAGTTATCCCCCAGGTACCTGGGAGCTACCCCATGCAGCCAGTC
                                                                                                                             TyrGlyGlnSerAsnTyrSerTyrProGlnValProGlySerTyrProMetGlnProVal
                                                                                                                                                                                        CCAGCCTATGGGCAGCAGCCAGCCACCTGCACCTACAAGACCGCAGGATGGAAACAAG
                                                                                                                                                                                                 ProAlaTyrGlyGlnGlnProAlaAlaThrAlaProThrArgProGlnAspGlyAsnLys
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MetAspArgGlyGlyPheGly 	lyGlyMetPheArgGlyGlyA 	.rgGlyGlyProGlyGlyMetA 	laProLyBProGluGlyPheL 	ProasnProGlyCysGlyasnG 	SerArgGlyAsnProSerGlyG 	lyargMetGlyGlyArgGlyG 	lyMetProProProLeuArgG 	laarglyslysProProMetA 	laAlaValGluTrpPheAspG 	luThrGlyLy8ProLy8GlyA AAACAGGAAAGCCCAAAGGCG	lyValValLy8MetA8nLy8A 	alGlnGlyLeuAsnAspSerV 	AspLeuAspLeuGlyProProV 	lySerAlaGlyGluArgGlyG 	lyglypheaspargGlyglym 	heSerGlyProGlyGluAsnA TTTCCGGACCAGGAGAGAACC	erSerPheArgGlnAspHisP 	
\metaspargG1\g1\pheG1\g1\q1\q1\q1\q1\q1\proG1\q1\proG1\q1\pro\q1\pro\q1\pro\q1\q1\q1\q1\q1\q1\q1\q1\q1\q1\q1\q1\q1\	GlyglymetPheargGlyGlyargGlyGlyAspargGlyGlyPhe-argGlyGlyArgGl 	argglyglyfroglyglymetargglyglyargglyglyteumetabpargglyglyfr 	AlaProLyBProGluGlyPheLeuProProProPheProProProGlyGlyAspArgGly 	roasnProGlyCysGlyAsnGlnAsnPheAlaTtpArgThrGluCysAsnGlnCysLy 	erargGlyasnProSerGlyGlyGlyAsnValGlnHisargAlaGlyAspTrpGlnCys 	GlyargmetGlyGlyargGlyGlyaspargGlyGlyPheProProArgGlyProArgGly 	GlymetProProProLeuargGlyGlyProGlyGlyProGlyGlyProGlyGlyProMet 	AlaargLybLybProProMetAbnSerMetArgGlyGlyLeuProProArgGluGlyArg 	AlaalavalglutrppheaspglyLybasppheglnglySerLysLeuLysValSerLeu 	GluThrGlyLysProLysGlyAspAlaThrValSerTyrGluAspProProThrAlaLys 	GlyVallyBMetAsnlyBArgThrGlyGlnDroMetIleHisIleTyrLeuAspLyB 	valGlnGlyLeuAsnAspServalThrLeuAspAspLeuAlaAspPhePheLysGlnCy 	pLeuAspLeuGlyProProValAspProAspGluAspSerAspAsnSerAlaIleTyr 	GlySeralaGlyGluargGlyGlyPheAsmLysProGlyGlyProMetAspGluGlyPro 	G1yG1yPheAbpArgG1yG1yMetSerArgG1yG1yArgG1yG1yG1yArgG1yG1yMet 	PheSerGlyProGlyGluAsnArgSerMetSerGlyProAspAsnArgGlyArgGlyArg 	SerSerPheArgGlnAspHisProSerSerMetGlyValTyrGlyGlnGluSerGlyGly 	
GlyProProGlyPr	ArgGlyGlyArgGl cgregregccegeg	.spArgGlyGlyPro ATCGTGGTGGTCCC	Particular Par	YBABNG1nCYBLYB GCAACCAGTGTAAG	lyaspTrpGlnCys agacTGGCAGTGT	rgGlyProArgGly aGGACCCCGGGGT	roGlyGlyProMet CTGGGGGACCCATG	roArgGluGlyArg cccgrgagggcaga	euLysValSerLeu TRAAGTCTCCCTT	roProThrAlaLys ACCCACTGCCAAG	leTyrLeuAspLys TCTACCTGGACAAG	hePheLysGlnCys TCTTTAAGCAGTGT	snSerAlaIleTyr ACAGTGCAATTTAT		lyargGlyGlyMet gacgcgGTGGaaTG	•		
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FEATURES

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 667 Location/Qualifiers

gi: 6679714

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RS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Schaefer, C.M., Schuler, G.D.,

Altechul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Willalon, D.K., Muzny, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Schwutz, J., Myers, R.M.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                           CONTACT: MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library Preparation: M. Bento Soares, University of Iowa
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and Dr.
Thomas L. Casavant.
Web site: http://genome.uiowa.edu
Contact: bento-soares@niowa.edu; tom-casavant@uiowa.edu
Bonaldo, M. F., Akabogu, I., Bair, T., Bair, J., Crouch, K., Davis, A.,
Fishler, K., Keppel, C., Kucaba, T., Lebeck, M., Melo, A., Schaefer, K.,
Scheetz, T., Smith, C., Snir, B., Tack, D., Trout, K., Walters, J.,
Casavant, T., Soares, M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1868
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (30-MAR-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: Plate: Row: Column: 0
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Director MGC Project.
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Best Local Similarity:
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MetAlaSerThrAspTyrSerThrTyrSerGlnalaAlaAlaGlnGlnGlyTyrSerAla
                                                          ACCACTGCTACAGTCACCACAACGCAGGCCTCTTACGCAGCTCAGACTGCATATGGCACC
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                                                                                   Plougastel, B., Mattei, M.G., Thomas, G. and Delattre, O. Cloning and chromosome localization of the mouse Ews Genomics 23 (1), 278-281 (1994)
                                                                                                                                                                                                         X79233.1 GI:488512
EWS gene.
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Tumeurs-Inst. Curie, 26 rue d'Ulm, 75231 Paris, Cedex 05, FRANCE
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/db_xref="GOA:Q61545"
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/chromosome="11"
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1	Indels:	98.31%	Query Match:
4.	Mismatches:	98.02%	Best Local Similarity:
00	Conservative:	99.24%	Percent Similarity:
643	Matches:	3571.50	Score:
2188	Length:	1.58e-75	Pred. No.:
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US-10-791-017A-2 (1-656) x MMEWS (1-2188)

¥	1 MetAlaSerThrAspTyrSerThrTyrSerGlnAlaAlaAlaGlnGlnGlyTyrSerAla 20	
8	57 ATGGCGTCCACGGATTACAGTACCTATAGTCAAGCTGCAGCCCAGCAGGGCTACAGTGCT 116	
¥	21 TyrThrAlaGlnProThrGlnGlyTyrAlaGlnThrThrGlnAlaTyrGlyGlnGlnSer 40	
ቻ	117 TACACCGCCCAGCCAACTCAAGGATATGCACAGACCACCCAGGCATATGGGCAACAAAGC 176	
¥	41 TyrGlyThrTyrGlyGlnProThrAspValSerTyrThrGlnAlaGlnThrThrAlaThr 60	
ਝ	177 TATGGAACCTATGGACAGCCTACTGATGTCAGCTATACTCAGGCTCAGACCACTGCCACC 236	
¥	61 TyrGlyGlnThrAlaTyrAlaThrSerTyrGlyGlnProProThrGlyTyrThrThrPro 80	
ъ	237 TACGGGCAGACTGCATATGCAACTTCTTACGGACAGCCTCCCACTGGTTATAGTACTCCA 296	
Ϋ́	81 ThrAlaProGlnAlaTyrSerGlnProValGlnGlyTyrGlyThrGlyAlaTyrAspThr 100	
ਝ	297 ACTGCCCCCCAGGCGTACAGCCCAGCCTGTGCAGGGATATGGCACTGGGGCTTATGACAGC 356	
Ϋ́	101 ThrThrAlaThrValThrThrThrGlnAlaSerTyrAlaAlaGlnSerAlaTyrGlyThr 120	
ř	357 ACCACTGCTACAGTCACCACAACGCAGGCCTCTTACGCAGCTCAGTCAG	
¥	121 GlnProAlaTyrProAlaTyrGlyGlnGlnProAlaAlaThrAlaProThrArgProGln 140	
ř	417 CAGCCTACCCACCTATGGCCAGCCAACAGCCACCGCACCCTACCAGACCACAG 476	
ਝ	141 AspGlyAsnLysProThrGluThrSerGlnProGlnSerSerThrGlyGlyTyrAsnGln 160	

5 0	α—α	
480 1493	461 ArgGluGlyArgGlyMetProProProLeuArgGlyGlyProGlyGlyProGlyGlyPro	
460 1433	41 LysValSerLeuAlaArgLysLysProProMetAsnSerMetArgGlyGlyLeuProPro	
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360 1133	341 AspGluGlyProAspLeuAspLeuGlyProProValAspProAspGluAspSerAspAsn 	
340 1073	21 ArgGlyGlyMetGlySerAlaGlyGluArgGlyGlyPheAsmLysProGlyGlyProMet	
320 1016	301 GlyargGlyargGlyGlyPheAspArgGlyGlyMetSerArgGlyGlyArgGlyGlyGlyGly	
300 956	281 GluSerGlyGlyPheSerGlyProGlyGluAsnArgSerMetSerGlyProAspAsnArg 	
280 896	261 TyrGlyGlnGlnSerSerPheArgGlnAspHisProSerSerMetGlyValTyrGlyGln	
260 836	241 ProProGlnThrGlySerTyrSerGlnAlaProSerGlnTyrSerGlnGlnSerSerSer	
240 776	221 GlyGlnGlnSerSerTyrGlyGlnGlnSerSerTyrGlyGlnGlnProProThrSerTyr 	
220 716	201 ThrSerTyrAspGlnSerSerTyrSerGlnGlnAsnThrTyrGlyGlnProSerSerTyr 	
200	181 MetGlnProValThrAlaProProSerTyrProProThrSerTyrSerSerThrGlnPro	
180 596	1 ProSerLeuGlyTyrGlyGlnSerAsnTyrSerTyrProGlnValProGlySerTyrPro	
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Search completed: February 21, 2005, 02:07:17 Job time : 7076.69 secs

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Command line parameters:

-MODEL-frame+ p2n.model -DEV-xlp
-MODEL-frame+ p2n.model -DEV-xlp
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-Q-/Ggn2_1/USBTO_gpool_p/US10791017/runat_17022005_125806_22064/app_query.fasta_1.1358
-DB-N_Geneseq_16Dec04 -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LAOPCL=0
-LOOPEXT=0 -UNITS=blts -START=1 =ND=-1 -MATRIX=blooum62 -TRANS-human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE-pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-NODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-NO MMAP -LARGEQÜERY -NEG_SCORES=0 -MAIT -DSPELOCK=100 -LONGLOG
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ABN97274	ABK84628 ABK64822	ADQ86032	3633 100.0 2371 2 AAQ50643	ID	
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ALIGNMENTS

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RESULT 1
AAQ50643
                                     AAQ50643;
25-MAR-2003
26-MAY-1994
                                                             AAQ50643 standard; cDNA; 2371 BP:
(revised)
(first entry)
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Human Ews gene clone BF1AC5 from foetal brain cDNA library.

chromosomal translocation; chimeric; chimaeric; Ewing sarcoma; Ews gene; malignant melanoma; hum-fli-1; primitive peripheral neuroectodermal tumour; human chromosome 11; numan chromosome 22; 88.

PN	Y P P	FT	ŦΤ	FΤ	ĘŢ	ΡŢ	ΡT	PH	×	သ	×	Ş	Ş	ξ	Ş	ğ	DE	ğ	ΡŢ	ij	ğ	AC	ğ	IJ,
WO9323549-A2.	polyA_signal 23312336 /*tag= c		•	/transl except= pos:17291731; aa:Val	/product= "EWS_protein"	/*tag= a	CDS 251995	Key Location/Qualifiers		Homo sapiens.			primitive peripheral neuroectodermal tumour; human chrom		chromosomal translocation; chimeric; chimaeric; Ewing sa		Human Ews gene clone BF1AC5 from foetal brain cDNA libra		26-MAY-1994 (first entry)	25-MAR-2003 (revised)		AAQ50643;		AAQ50643 standard; cDNA; 2371 BP:

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Thomas G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The probes 22RR3 and 22RR12 were used to screen a human foetal brain cDNA library (Stratagene cat.# 936206). The clone BFLAC5 was identified and sequenced. It represents the entire coding region and 3'-UTR of the Ewsgene. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid of EWS gene and its hybrid(s) - contg. gene sequence involved in chromosomal trans-location, also derived mRNA, probes, fusion proteins etc., for diagnosis and treatment of Ewing sarcoma and melanoma.
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                         The present invention describes an isolated tumour-associated antigenic target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of (a); (c) the complement of (a) or (b); (d) a sequence that has 80% sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-(c). Also described: (1) an expression vector comprising the above nucleic acid, (2) a host cell comprising the above expression vector; (3) a process for producing a polypeptide; (4) an isolated polypeptide comprising: (a) an amino acid sequence encoded by the full-length coding region of the above nucleotide sequences; (b) an amino acid sequence encoded by the full-length coding region of the above nucleotide sequences; or (c) a sequence having at least 80% identical to (a) or (b); (5) a chimeric polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid molecule and encoded polypeptide, for diagnosing, preventing or treating cell proliferative disorders such as cancer
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cc an isolated antibody that binds to the above polypeptide; (7) a process for producing the antibody; (8) an isolated oligopeptide that binds to the above polypeptide; (9) a tumour-associated antigenic target (TAT) binding organic molecule that binds to the above polypeptide; (10) a composition of matter comprising the above (chimeric) polypeptide, (10) a composition of matter comprising the above (chimeric) polypeptide, (11) an article of manufacture comprising a container and the composition of matter contained within the container; (12) methods of the cell is at least in part dependent upon a growth of the cell is at least in part dependent upon a growth (12) therapeutically treating a mammal having a cancerous tumour comprising (13) the protein in a sample suspected of containing the protein (14) a method of determining the companie of a protein in a sample suspected of containing the protein (16) a method for treating or preventing a cell proliferative (17) a method of binding an antibody, oligopeptide or organic molecule to a cell that expresse the protein described above. The TAT sequences have cytostatic activities, and can be used in gene therapy. The composition and methods are useful for diagnosing. C preventing or treating cancer. The composition is also used for preparing cell proliferative disorder or cancer. The present sequence represents a cell proliferative disorder or cancer. The present sequence represents a cell proliferative disorder or cancer. The present sequence represents a cell proliferative disorder or cancer. The present sequence represents a cell proliferative disorder or cancer. The present sequence represents a cell proliferative disorder or cancer. The present sequence represents a cell proliferative disorder or cancer. The present sequence represents a cell proliferative disorder or cancer. The present sequence represents a cell proliferative disorder or cancer. The present sequence represents a cell proliferative disorder or cancer. The present sequence represents a cell prol

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US-10-791-017A-2 (1-656) x ADQ86032 (1-2372)		Query Match:	imilarity:		Score:	Pred. No.:	***************************************
) x ADQ86032	13	100:00%	100.00%	100.00%	3633.00	1.69e-116	
(1-2372)	Gaps:	Indels:	Mismatches:	Conservative:	Matches:	Length:	
	0	0	0	0	656	2372	

583	CCCAGCCTAGGATATGGACAGAGTAACTACAGTTATCCCCAGGTACCTGGGAGCTACCCC	. 524	문
180	ProSerLeuGlyTyrGlyGlnSerAgnTyrSerTyrProGlnValProGlySerTyrPro	161	S
523	GATGGAAACAAGCCCACTGAGACTAGTCAACCTCAATCTAGCACAGGGGGTTACAACCAG	464	탕
160	AspGlyAsnLysProThrGluThrSerGlnProGlnSerSerThrGlyGlyTyrAsnGln :	141	S
463	CTGCTTATCCAGCCTATGGGCAGCCAGCCAGCAGCCACCTACAAGACCGCAG	404	밁
140	GlnProAlaTyrProAlaTyrGlyGlnGlnProAlaAlaThrAlaProThrArgProGln	121	Ş
403	ACCACTGCTACAGTCACCACCCAGGCCTCCTATGCAGCTCAGTCTGCATATGGCACT	344	밁
120	ThrThrAlaThrValThrThrGlnAlaSerTyrAlaAlaGlnSerAlaTyrGlyThr	101	ફ
343	ACTGCCCCCAGGCATACAGCCAGCCTGTCCAGGGGTATGGCACTGGTGCTTATGATACC	284	밁
100	ThrAlaProGlnAlaTyrSerGlnProValGlnGlyTyrGlyThrGlyAlaTyrAspThr	81	Ş
283	TATGGGCAGACCGCCTATGCAACTTCTTATGGACAGCCTCCCACTGGTTATACTACTCCA	224	문
08	TyrGlyGlnThrAlaTyrAlaThrSerTyrGlyGlnProProThrGlyTyrThrThrPro	61	Ş
223	TATGGAACCTATGGACAGCCCACTGATGTCAGCTATACCCAGGCTCAGACCACTGCAACC	164	당
60	TyrGlyThrTyrGlyGlnProThrAspValSerTyrThrGlnAlaGlnThrThrAlaThr	41	Ś
163	TACACCGCCCAGCCCACTCAAGGATATGCACAGACCACCCAGGCATATGGGCAACAAAAGC	104	밁
40	TyrThrAlaGlnProThrGlnGlyTyrAlaGlnThrThrGlnAlaTyrGlyGlnGlnSer	21	Ş
103	ATGGCGTCCACGGATTACAGTACCTATAGCCAAGCTGCAGCGCAGCAGGGCTACAGTGCT	44	당
20	MetAlaSerThrAspTyrSerThrTyrSerGinAlaAlaAlaGlnGlnGlyTyrSerAla	1	Ş

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ABK84628 standard; cDNA; 2390 쁑

ABK84628

14-AUG-2002 (first entry)

cDNA differentially expressed in granulocytic cells

Human; 88; granulocytic cell; DNA chip; bacterial infection; viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease; Crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.

Homo sapiens.

WO200228999-A2

11-APR-2002

03-OCT-2001; 2001WO-US030821.

03-OCT-2000; 2000US-0237189P

Beazer-Barclay Y, Weissman MS, Yamaga ູດ Vockley

2002-435328/46.

Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and drug toxicity.

Claim 1; SEQ ID NO 1199; 114pp; English

The invention relates to detecting (M1) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (Gs) identified DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated GC, where differential expression of Gs is indicative of GCA. Also included are modulating (M2) GA by contacting GC with an agent that alters the expression of at least one gene in Gs; (2) screening (M3) for an agent capable of modulating GCA or an inflammation (especially chronic) in a à

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The invention relates to a method of diagnosing (I) the onset or progression of benign prostatic hyperplasia (BPH), or screening (II) for or identifying an agent that modulates the onset or progression of BPH. The method is based on changes in gene expression in BPH tissue isolated from patients exhibiting different clinical states of prostate hyperplasia as compared to normal prostate tissue. (I) comprises detecting the expression levels of one or more genes in prostate cells from the subject that are differentially regulated compared to normal prostate cells. (II) comprises preparing a first gene expression profile of BPH cells or BPH-like cell population, exposing the cells to the
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JAPAN TOBACCO INC.
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agent, preparing a second gene expression profile of the agent exposed cells, and comparing the first and second gene expression profiles. (I) is useful for diagnosing the onset or progression of BPH. (II) is useful for identifying an agent that modulates the onset or progression of BPH.

The methods are useful to present information identifying the expression level in a tissue or cells, by comparing the expression level of genes given in the specification in the tissue or cells to the level of expression of gene in the database, and displaying the expression levels of at least one gene in the tissue or cell sample compared to the expression level in BPH. Agents using (II) are useful for treating BPH or prostate cancer. ABK64106-ABK64860 represent human benign prostatic hyperplasia gene sequences of the invention
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Sequence 2390 BP; 645 A; 589 Ç 668 G; 488 T; 0 U; 0 Other;

F	Ş	Дb	Q	Дb	Ş	Db	Ş	Db	8	망	Q	Db	Q	Db	Q	Db	Ş	Db	Q	Дb	Q	Дb	Ş	US-10-791	Pred. No.: Score: Score: Percent Sim: Best Local (Query Match DB:	3 1 4 cm
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ABN97274 standard; DNA; 2390 ₽P 문 S 밁 S 밁

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음 중 음

13-AUG-2002 ABN97274; (first entry)

Gene #3772 used ő diagnose liver cancer

Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic; metastatic liver tumour; cytostatic; expression profile; disease state; disease progression; drug toxicity; drug efficacy; drug metabolism.

Homo sapiens.

WO200229103-A2

11-APR-2002

02-OCT-2001; 2001WO-US030589

02-OCT-2000; 2000US-0237054P

(GENE-) GENE LOGIC

Horne 'n Alvares C, Peres-Da-Silva ß Vockley JG,

WPI; 2002-426119/45.

Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a patient, involves detecting the level of expression of two or more genes in a liver tissue sample.

Claim ۲. SEQ ID NO 3772; 298pp; English.

RRESULT 5
ARMS97575
ARMS976757
ARMS9767
ARMS9 The invention relates to a novel method for diagnosing and detecting the corporession of liver cancer, hepatocellular carcinoma or metastatic liver tumour in a patient, and differentiating metastatic liver cancer from the patocellular carcinoma in a patient, involving detecting the level of expression of two or more genes represented in ABN93503-ABN97455 in a constant cartivity. The method of the invention has hepatotropic, and the progression of liver cancer, hepatocellular carcinoma and metastatic the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying capression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, drug toxicity, drug efficacy and drug metabolism. Note: The sequence data cobtained in electronic format directly from WIPO at fig.wipo.int/pub/published_pct_sequences

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Sequence 2390 BP; 645 A; 589 Ç 668 G; 488 T; 0 U; 0 Other;

DB:	Query Match:	Best Local Similarity:	Percent Similarity:	Score:	Pred. No.:	Alignment Scores:
6	100.00%	100.00%	100.00%	3633.00	1.7e-116	
Gaps:	Indels:	Mismatches:	Conservative:	Matches:	Length:	
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                                  Human cDNA encoding the Ewing sarcoma protein SeqID 1.
human; ss; gene; Ewing sarcoma; EWS; prostatic cancer; alopecia; acne; hypogonadism; androgen-resistance syndrome; testicular feminisation.
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                                                                                                                                                                                                                                                                                                                                              This invention relates to a novel modulators that alter the interaction CC between the Ewing sarcoma protein (EWS) and its nuclear receptor, as well CC as the screening method thereof. Specifically, it refers to determining CC and identifying a hormonal effect brought about by test compounds that CC modulate either the binding of EWS to the nuclear receptor or the ligand-induced activity of this receptor. The present invention describes the CC nuclear receptors as including osetrogen, progesterone, thyroid hormone, CC vitamin D, and retinoic acid receptors, most preferably they are androgen CC receptors. Accordingly, these modulators may be used in the development CC diseases associated with receptor dysfunction such as prostatic cancer, CC alopecia, acne, hypogonadism and androgen-resistance syndrome e.g. CC simple, inexpensive and rapid assessment of the hormonal effects of these test compounds. This method provides reliable, sensitive, CC test compounds. This polynucleotide sequence is the cDNA encoding the Numan Ewing sarcoma protein of the invention.
                                                                                                                                                                                                                                                                                                                           Sequence 2390 BP; 646 A; 589 C; 668 G;
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Tumour-associated antigenic target; TAT; human; overexpression; c tumour; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoma; leukaemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping;
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2004-347921/32.
                                       GENENTECH INC.
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New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or prostate cancer or tumor.

Claim 1; SEQ ID NO 5989; 7273pp; English

mammals. The invention also relates to nucleic acid and polypeptide sequences at least 80% identical to the TAT nucleic acids and polypeptides; expression vectors and host calls comprising a TAT nucleic acid; an antibody specific for a TAT polypeptide; a peptide or organic molecule which binds to a TAT polypeptide; fusion proteins comprising a TAT polypeptide; and methods and compositions for the treatment or diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder cancer, pancreatic cancer, cervical cancer, cancers of the central nervous system, melanoma and leukaemia. TAT nucleic acids may further be used as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence The invention relates to human tumour associated antigenic target (TAT) polypeptides, and their related nucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in

Sequence 2390 BP; 645 A; 589 Ç 668 G; 488 T; 0 U; 0 Other;

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Percent Similarity:
Best Local Similarity:
       Query
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US-10-791-017A-2 (1-656) x ACN40903 (1-2390)

S 밁 S . 뭐 Ś 吊 S 밁 8 밁 S Ś 밁 101 284 224 164 104 121 81 61 41 21 44 ${\tt GlnProAlaTyrProAlaTyrGlyGlnGlnProAlaAlaThrAlaProThrArgProGln}$ ThrThrAlaThrValThrThrThrGlnAlaSerTyrAlaAlaGlnSerAlaTyrGlyThr ThrAlaProGlnAlaTyrSerGlnProValGlnGlyTyrGlyThrGlyAlaTyrAspThr TyrGlyGlnThrAlaTyrAlaThrSerTyrGlyGlnProProThrGlyTyrThrThrPro TyrGlyThrTyrGlyGlnProThrAspValSerTyrThrGlnAlaGlnThrThrAlaThr TACACCGCCAGCCCACTCAAGGATATGCACAGACCACCCAGGCATATGGGCAACAAAGC TyrThrAlaGlnProThrGlnGlyTyrAlaGlnThrThrGlnAlaTyrGlyGlnGlnSer MetAlaSerThrAspTyrSerThrTyrSerGlnAlaAlaAlaAlaGlnGlnGlyTyrSerAla TATGGGCAGACCGCCTATGCAACTTCTTATGGACAGCCTCCCACTGGTTATACTACTCCA TATGGAACCTATGGACAGCCCACTGATGTCAGCTATACCCAGGCTCAGACCACTGCAACC ATGGCGTCCACGGATTACAGTACCTATAGCCAAGCTGCAGCGCAGCAGGCTACAGTGCT **ACTGCCCCCAGGCATACAGCCAGCCTGTCCAGGGGTATGGCACTGGTGCTTATGATACC** 140 120 343 100 283 80 223 60 163 40 103 20 403

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The present invention relates to the isolation of novel cDNA sequences which encode human secreted proteins. The cDNA sequences have been

Claim 1;

Page 100; 391pp; English

New polynucleotides encoding secreted asthma, HIV and Crohn's disease.

proteins

useful

for

treating

WPI; 2002-010900/01.

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Gulukota
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K, Graham
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             derived from a variety of human tissues. The invention also provides a method for producing proteins from these polynucleotide sequences. The proteins are useful for identifying compounds that modulate their activity and production, and the cell is also useful for identifying compounds that modulate expression of the polynucleotide sequences encoding the secreted proteins. The sequences of the invention are useful for treating diseases such as hyperproliferative disorders (e.g. cancer), inmune deficiency disorders (e.g. severe combined immunodeficiency (SCID)), autoimmune disorders (e.g. multiple sclerosis), blood disorders (e.g. thrombocytopaenia), inflammatory disorders (e.g. arthritis) and infectious disorders (e.g. hepatitis). The polynucleotide sequences of the invention are also useful in gene therapy. AAS62214-AAS62838
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Percent Similarity:
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                                                                                                                                                  The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (1) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (1). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia, occlusive ischaemia or vassospastic ischaemia) by measuring expression levels of particular genes (ABI99202 to ABI9912, encoding the protein sequences in ABB57020 to ABB57374) or by determining the expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition improving drugs or therapeutics for ischaemic diseases. ABI9913 and ABI9914 represent primers for a mouse ischaemic condition related sequence, which are used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
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Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
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30-MAR-2001; 2001WO-US008631.

11-OCT-2001.

31-MAR-2000; 2000US-00540217. 23-AUG-2000; 2000US-00649167.

(HYSE-) HYSEQ INC.

RT, Liu C, Tang Ţ

2001-639362/73.

New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity. mutations

Claim 1; SEQ ID NO 6451; 103pp; English.

The invention relates to isolated polynucleotide (I) and polypeptide (II) casequences. (I) is useful as hybridisation probes, polymerase chain (CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping, CC and in recombinant production of (II) The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal CC useful for generating antibodies against it, detecting or quantitating a CC useful for generating antibodies against it, detecting or quantitating a CC useful for generating antibodies against it, detecting or quantitating a CC useful for generating antibodies against it, detecting or quantitating a CC supplement. (II) and its binding partners are useful in medical imaging CC involving aberrant protein expression or biological activity. The CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other triats to assess biodiversity and to produce other types of data and products dependent on DNA and CC coding sequences of the invention. Note: The sequence data for this CC coding sequences in the printed specification, but was obtained in CC coding sequences in the printed specification, but was obtained in CC celetronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 2388 BP; 628 A; 599 C; 668 G; 493 7 0 U; 0 Other;

Percent Similarity:
Best Local Similarity:
Query Match: Alignment Scores: Мо :: 5.11e-113 3531.50 98.64% 98.34% 97.21% Gaps: Conservative: Mismatches: Indels: 2388 651 2 3 6

US-10-791-017A-2 (1-656) x AAS70647 (1-2388)

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AAS62623 standard; CDNA; 2273 ₽P

AAS62623

14-FEB-2002 (first entry)

cDNA sequence #410 encoding novel human secreted protein

RESULT 11
AAS62623/c
ID AAS626:
XX AAS626:
XX AC AAS626:
XX DE CDNA so
XX Human of infect.
XX immune
XX im Human secreted protein; hyperproliferative disorder; autoimmune disorder; immune deficiency disorder; blood disorder; inflammatory disorder; infectious disorder; gene therapy; antimicrobial; hepatotropic; immunosuppressive; antirheumatic; ss.

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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polynucleotides encoding secreted proteins useful for asthma, HIV and Crohn's disease.
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 TrpGlnCysProAsnProGlyCysGlyAsnGlnAsnPheAlaTrpArgThrGluCysAsn
                                                                                                        GGACCCATGGGTCGCATGGGAGGCCGTGGAGGAGATAGAGGAGGCTTCCCTCCAAGAGGA
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exon	on	FT 1NCTON 246305 FT /*tag= f FT /number= 3 FT exon 306429	i kon		/*t /nu /nu 134	/*: /nu exon 97	FT /numbers 1 FT /codon_starts 2527 FT intron 38 96	Key Location 137	OS Homo sapiens.	 KW chromosomal translocation; chimeric; chimaeric; Ewing sarcoma; Ews gene; KW malignant melanoma; hum-fli-1; KW primitive peripheral neuroectodermal tumour; human chromosome 11; KW human chromosome 22; 68. 		DT 25-MAR-2003 (revised) DT 26-MAY-1994 (first entry)	AX AC AAQ50646; YY	SULT 12 Q50646 AAQ50646	Qy 642 MethsplysGlyGluHisArgGlnGluArgArgAspArgProTyr 656	Qy 622 ProGlyProLeuMetGluGlnMetGlyGlyArgArgGlyGlyArgGlyGlyProGlyLys 641	Qy 602 GlyArgGlyMetAspArgGlyGlyPheGlyGlyGlyArgArgGlyGlyProGlyGlyPro 621	577 GGTGGTCCCGGTGGAATGTTCAGAGGTGGCCGTGGTGGAGACACAGAGGTGGCTTCCGTGGT	582	QY 562 AspArgGlyArgGlyBroGlyGlyMetArgGlyGlyArgGlyGlyLeuMetAspArg 581	646 CAGTGT	Db 706 TGGCAGTGTCCCAATCCGGGTTGTGGAAACCAGAACTTCGCCTGGAGAACAGAGTGCAAC 647 OV 542 GlnCysLysAlaProlysBroGluGlyPheLeuProProProProProProProProFixGlyGly 561	
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Qy 25 ProThrGlnGlyTyrAlaGlnThrThr Db 216 CCCACTCAAGGATATGCACAGACCACCAGTA Qy 34GlnAla' Qy 34	DB: 2 Gaps: US-10-791-017A-2 (1-656) x AAQ50646 (1-3309) Qy 5 AspTyrSerThrTyrSerGlnAlaAlaAlaGlnGlnGly Db 96 GATTACAGTACCTATAGCCAAGCTGCAGCGCAGCAGGGGG Qy 18	at ce di	CC The intron-exon junctions of the CC have been sequenced (see AAQ50646 CC different fusion products which c CC two genes, as happens after speci CC predicted (see AAQ50671-Q50678). CC other observed translocations are CC other observed translocations are CC 3309 residue sequence AAQ50646 do CC is a combination of the Ews cDNA CC individual intron sequences with CC (Undated on 25-MAR-2003 to correct CC (Undated on 25-MAR-2003 to correct CC)	P-PSDB; AAR44555. New nucleic acid of EWS involved in chromosomal proteins etc., for diagnostic bisclosure; Fig 6 and F	PF 19-MAY-1993; 93WO-FR000494. XX PR 20-MAY-1992; 92FR-00006123: XX PA (CNRS) CNRS CENT NAT RECH SCI. XX PI Aurias A, Delattre O, Desmaze C, PI Thomas G, Zucman J;	
CAGGTAATCTTTAAAATAATTACATGTAGCTGC 275 GlnAlaTyrGlyGlnGlnSerTyrGlyThrTyr 44		B57 G; B55 T; O U; O Other; Length: 3309 Matches: 652 Conservative: 0 Mismatches: 0	The intron-exon junctions of the human Ews gene and the Hum-Fli-1 gene have been sequenced (see AAQ50646 and AAQ50662, respectively). The different fusion products which could be formed by fusing exons from the two genes, as happens after specific chromosomal translocations, can be predicted (see AAQ50671-Q50678). The sequences at fusion junctions of other observed translocations are given in AAQ50679-Q50683). NOTE: the 3309 residue sequence AAQ50646 does not appear in the specification; it is a combination of the Ews cDNA sequence (Fig 6, AAQ50643) and the individual intron sequences with their intron-exon junctions (Fig 12). (Updated on 25-MAR-2003 to correct FN field.)	gene and its hybrid(s) - contg. gene sequence trans-location, also derived mRNA, probes, fusion nosis and treatment of Ewing sarcoma and melanoma.	Melot T, Peter M, Plougastel B;	
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		205 GlnSerSerTyrSerGlnGlnAsnThrTyrGlyGlnProSerSerTyrGlyGlnGlnSer 224	816 TATGGACAGAGTAACTACAGGTTATCCCCAGGTACCTGGGAGCTACCCCATGCAGCCAGTC 875 185 ThralaProProSerTyrProProThr	138	ValThrThrGlnAlaSerTyrAlaAlaGlnSerAlaTyrGlyThrGlnProAlaTyrGllllllllllllllllllllllllllllllllllll	GGGTGAAATCTGATGCAGCGTCCCCCTTTGGTCTAGGTTATACTCCAACTGCCCCCAGAATCTGATGCAGCTCCCCCTTTGGTCTAGGTTATACTCCAACTGCCCCCCAGAATTYrSerGlnProValGlnGlYTyrGlYThrGlyAlaTyrAspThrThrAlaThrAll

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                                                                                                                   GCCCAAAGCCTGAAGGCTTCCTCCCGCCACCCTTTCCGCCCCCGGGTAGGTGCAGGTTT
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Alignment Scores:

Sequence 1988

BP; 519 A;

504 C;

584 G;

381 T; 0 U; 0 Other;

The present invention relates to novel human secretory or membrane proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-ADA54071). The coding sequences are useful in the gene therapy of diseases caused by abnormalities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease.

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XX ADA53
XX ADA53
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XX Cyton
CX Cyton
CX Infla
XX Gene
KW Gene
KW Infla
XX I1-M2
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24-JAN-2002; 2002US-0350435P.
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Hio Y, Otsuka K, Nagai K, Irie
Otsuka M, Nagahari K, Masuho Y;
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01 GlyArgGlyArgGlyGlyPh 	81 Gluse 84 GAGTC	61 TyrGlyGlnGlnSerSe 24 TACGGGCAGCAGAGTTO	41 ProProGlnThrGlyS	21 GlyGlnGlnSerSe	01 ThrSerTyrl	81 MetGlnPro	61 ProSe	41 As 16	21 GlnPr 72 CAGCC	01 ThrThrAl	81 ThrAlaProGln 52 ACTGCCCCCCAG	61 Tyrg	41 TyrglyTh	21 TyrThrAlaGlnP: 72 TACACCGCCCAGC	1 MetAlaSerThr 12 ATGGCGTCCACG	656	ž
GlyGlyPheAspArgGlyGlyMet 	rGlyGlyPheSerGlyProGly 	SerSerPheArgGlnAsp AGTTCATTCCGACAGGAC	CCTTY Y	SerTyrGlyGlnGlnSer 	ABDG1nSerSerTyrSer 	ValThrAlaProProSerTyrPro	rLeuGlyTyrGlyGlnSerAsnTyrSerTyrProGlnValProGlyS	pGlyAsnLysProThrGluThrSerGlnProGlnSerSerThrGlyGlyTyrAsnGln	oAlaTyrProAlaTyrGlyGlnGlnProAlaAlaThrAlaProThrArgProGln TGCTTATCCAGCCTATGGGCAGCAGCCAGCAGCCCCCCA	aThrValThrThrThrGlnAlaSerTyrAlaAlaGlnSerAlaTy 	31nAlaTyrSerGlnPro 	SGCAGACCGCCTATGCAACTTCTTA	rTyrGlyGlnProThraspValSerTyrThrGlnalaGlnThrThrAl 	ProThrGlnGlyTyr CCCACTCAAGGATAT	aSerThrAspTyrSerThrTyrSerGlnAlaAlaAlaGlnGlnGlyTyrSerA 	506 (1	2.35e-104 Le 3277.00 : Ma 91.31% Co 91.31% M1
GlyGlyMetSerArç GAGGCATGAGCAG <i>I</i>	roglygluasnargSerMetSerGly 	Hisproser	rSerGlnAlaProSerGlnTyrSerGlnG CAGCCAAGCTCCAAGTCAATATAGCCAAC	SerSerTyrGlyGlnGlnPro 	:rGlnGlnAsnThrTyrGlyGlnP 	ProThrs	TyrSerTyrProGlr	GlnProGlnSerSer	GlnProAlaAlaThr CAGCCAGCAGCCACT	AlaSerTyrAlaAla GCCTCCTATGCAGCT	SerGlnProValGlnGlyTyrGly	TyrGlyGlnProPro TATGGACAGCCTCCC	ValSerTyrThrGlr grcagctatacccae	roThrGlnglyTyrAlaglnThrThrGlnalaTyrGlyG 	SerGlnAlaAlaAla agccaagcTgcagcc		Length: 198 Matches: 599 Conservative: 0 Mismatches: 1
SerArgGlyGlyArgGlyGlyGl 	ProAs	SerMetGlyValTyrGlyGln aGCATGGGTGTTTATGGGCAG	SerGlnGlnSerSerS	G nProProThrSerTy CAGCCTCCCACTAGTTAK	GlyGlnProSerSerTy GGCAACCGAGCAGCTA	erTyrSerSerThrGln CTATTCCTCTACACAG	WalProGlySerTyrP	ThrGlyGlyTyrAsr	AlaProThrArgPro	GInSerAlaTyrGlyThi CAGTCTGCATATGGCACT	yrGlyThrGlyAlaTyrAspT 	rglyglnProProThrglyTyrThrThr rggacagccrcccactggttatactact	AlaGlnThrThrAla CTCAGACCACTGCA	AlaTyrGlyGlnGlnSer GCATATGGGCAACAAAGC	GlnGlnGlyTyrSer cagcagggcTacagr		9 88 ·
YG1Y 320 AGGA 803	эрАвлАгд 300 \TAACCGG 743	yGln 280 - - 683	rSer 260 CAGC 623	TYF 240	rTyr 220 CTAT 503	nPro 200 CCG 443	rPro 180 416	nGln 160 416	oGln 140	Thr 120 ACT 371	oThr 100 rACC 311	hrPro 80 CTCCA 251	laThr 60 CAACC 191	nser 40 AGC 131	rAla 20 GCT 71		
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                                                                                                                                                                                                                                                                       connections obtained by an oligo-capping method, where none of these continues are identical to any known human mRNAs. The present invention describes an immunoassay to identify agonists and antagonists, as well as antibodies, antisense molecules and siRNAs that can all be used to bind to and modulate expression of the cDNA molecules. As such, these molecules are useful for diagnostic markers or therapeutic targets for the various diseases or morbid states. In particular, they are useful in gene therapy for treating osteoporosis, neurological disease, Alzheimer's disease, dementia, short memory and various cancers, as well as for maintaining equilibrium of sense or motor function, and for treating emotional reaction, fear response and panic. Accordingly, they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian, cytostatic and tranquiliser activities. This polymucleotide is a full contain the sequence of the invention, MOTE: This sequence is not given in the sequence listing of the specification but can be obtained on CD-ROM from the Buropean Patent Office, Vienna Sub-office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           osteoporosis; neurological disease; Alzheimer's disease; Parkinson's disease; dementia; short memory; cancer; sense or motor function; emotional reaction; fear response; osteopathic; neuroprotective; nootropic; antiparkinsonian; cranquiliser.
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Wakamatsu
                                                                                                                                                                                                                                                  Sequence 2026 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention relates to novel, isolated full length human cDNA molecules and the encoded proteins thereof. Specifically, it refers to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New 1995 cDNA, useful for treating osteoporosis, neurological diseases, Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
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09-MAY-2003; 2003JP-00131452.
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                                                                       Tumour-associated antigenic target; TAT; human; overexpression; citumour; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoma; leukaemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping;
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The invention relates to human tumour-associated antigenic target (TAT) CC polypeptides, and their related nucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus CC serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide commands and treatment of cancer in the mammals. The invention also relates to nucleic acid and polypeptide compenses at least 80% identical to the TAT nucleic acids and complete acids and the sequences at least 80% identical to the TAT nucleic acids and complete comple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or
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Percent Similarity:
Best Local Similarity:
Query Match: 밁 გ 밁 8 US-10-791-017A-2 (1-656) x ACN37537 (1-2177) Мо :: 94 21 34 1 MetAlaSerThrAspTyrSerThrTyrSerGlnAlaAlaAlaGlnGlnGlyTyrSerAla TACAACACCCAGCCCACTCAAGGATATGCACAGACCACCCAGGCATATGGGCAACAAAGC TyrThrAlaGlnProThrGlnGlyTyrAlaGlnThrThrGlnAlaTyrGlyGlnGlnSer ATGGCATCCATGGATTACAGTACCTATAGCCAAGCTGCAGCGCAGCAGGGCTACAGTGCT 4.96e-102 3210.00 93.14% 91.16% 88.36% Conservative: Mismatches: Gaps: Indels: Length: 2177 598 13 45 2

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-MODEL=frame+ p2n.model pUSU-791017/runat 17022005 125808 22107/app query.fasta_1.1358
-Qs-(cgn2 1/USPTO_spool p/US10791017/runat 17022005 125808 22107/app query.fasta_1.1358
-DB=Issued Patents NA -QFMT=fastap -SUFFIX.p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=51ts -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-NO_MMAP -LARGEQUERY -NEG_SCORE=0 -WAIT -DSPELOCK=100 -LONGLOG
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US-09-919-039-322

US-09-919-016-16785

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Sequence 5044, Ap
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Sequence 18, Appl
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Sequence 322, Appl
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ALIGNMENTS

RESULT 1 US-08-343-443B-1

Application US/08343443B

Sequence 1, Applic Patent No. 5968734 APPLICANT: Desmaze, Chantal
APPLICANT: Melot, Thomas
APPLICANT: Peter, Martine
APPLICANT: Peter, Martine
APPLICANT: Ploougastel, Beatrice
APPLICANT: Thomas, Gilles
APPLICANT: Thomas, Gilles
APPLICANT: Tucman, Jessica
TITLE OF INVENTION: NUCLEIC ACID CORRESPONDING TO A GENE OF
TITLE OF INVENTION: CHROMOSOME 22 INVOLVED IN RECURRENT CHROMOSOMAL
TITLE OF INVENTION: TRANSLATIONS ASSOCIATED WITH THE DEVELOPMENT OF CANCEROUS
TITLE OF INVENTION: TRANSLACATIONS
TITLE OF INVENTION: TRANSLOCATIONS
TITLE OF INVENTION: TRANSLOCATIONS APPLICANT: COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: AEDIT 1.0 DOS text editor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/343,443B
FILLING DATE: 18-NOV-1994
CLASSIFICATION: 514 STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPB: Floppy disk NUMBER OF SEQUENCES: 129
CORRESPONDENCE ADDRESS:
ADDRESSE: Weiser & Associates
ATREET: 230 South Fifteenth Street
CITY: Philadelphia PRIOR APPLICATION DATA: Delattre, Olivie Desmaze, Chantal Aurias, Alain Olivier

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Percent Similarity:
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Query Match:
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2371 base pairs
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NAME/KEY:
LOCATION:
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REFERENCE/DOCKET NUMBER: 989.
TELECOMMUNICATION INFORMATION:
TELESPHONE: 215-875-8383
TELEFAX: 215-875-8394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/I
FILING DATE: 19-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9:
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ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
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TYPE: nucleic acid
STRANDEDNESS: double
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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; Sequence 5043, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REFERENCE: CL001107
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-30
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-0-08
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NUMBER OF SEQ ID NOS: 207012
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Sequence 5044, Application US/09949016

Patent NO. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES AS:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755
                                                                                                                                                        RESULT 4
US-09-949-016-5044
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PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.
SEQ ID NO 5044
LENGTH: 1785
TYPE: DAT
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-33
PRIOR FILING DATE: 2000-10-33
PRIOR FILING DATE: 2000-10-39
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PRIOR FILING DATE: 2000-10-30
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TOPOLOGY: 1:
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US-08-437-027-18
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                                                                                                                                                             CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 4641
TELECOMMUNICATION INFORMATION:
TELEFHONE 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 18:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:

APPLICANT: Landanyi, Marc
APPLICANT: Gerald, William
TITLE OF INVENTION: A DIAGNOSTIC TEST FOR TEST FOR THE DESMOPLASTIC
TITLE OF INVENTION: SMALL ROUND CELL TUMOR
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 2412 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: CO-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Cooper & Dunham LLP STREET: 1185 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: New York COUNTRY: U.S.A. ZIP: 10036
                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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US-09-919-039-322
Sequence 322, Application US, Patent No. 6727066; GENERAL INFORMATION: GENES R. APPLICANT: Kaser, Matthew R. TITLE OF INVENTION: GENES ED; FILE REFERENCE: PA-0035 US
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CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 60/222,113
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 401
SOFTWARE: PERL PROGram
SEQ ID NO 322
LENGTH: 1939
TYPE: DNA
CORGANISM: Homo sapiens
PEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 672706
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               CAGGGCTATGGACAGCAGAACCAGTACAACAGCAGCAGTGGTGGTGGAGAGGTGGAGGT-
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                                      SerSerTyrGlyGlnGlnSerSerTyrGlyGlnGlnSerSerTyrGlyGlnGlnProPro
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Db 31686 ACACTTCATACCCTTGAGAAACTTGATTATTAGAGTGAAGAAATTAAAAATTGTGTGTAG 31745	Db 31626 ACCACTCCGTGGAGGTACTTTTTCTGAGCTCCTATGTTGCATTAAAAGGTTTTCAGT 31685 Qy 472 472	Db 31566 GAAGCCTCCAATGAACAGTATGCGGGGTGGTCTGCCACCCCGTGAGGGCAGAGGCATGCC 31625 Qy 467 oProProLeuArgGly472	Db 31506 TTGTCTTGTTCCAĞĞĞAĀAĞĀTTTTCAAĞĞĞAĞCĀĀĀCTTĀAĀĞTCTCCCTĞĞTCĞĞAĀ 31565 Qy 447 BLYBProProMetABnSerMetArgGlyGlyLeuProProArgGluGlyArgGlyMetPr 467	Db 31461	Db 31405 TTAGAGAAGATTACAGGCAGACCTAATGCATCTGGGAGTGG-TCATTTGATGATGATCAT 31460 Qy 422 Thralalybalaalalglillilli	US-10-791-017A-2 (1-656) x US-09-949-016-16785 (1-35784) Qy	Best Local Similarity: 29.12% Mismatches: 11 Query Match: 26.37% Indels: 554 DB: 4 Gaps: 6	cores: 1.27e-41 Length: 958.00 Matches: 1.27e-41 Conservative:	; TYPE DNA ; TYPE DNA ; ORGANISM: Human US-09-949-016-16785	; NUMBER OF SEQ ID NOS: 207012 ; SOPTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 16785 . LENGTH: 35784		CURRENT FILING DATE: 2000-104-14 PRIOR APPLICATION NUMBER: 60/241,755 PRIOR APPLICATION NUMBER: 60/241,755	APPLICANT: VENTER, J. Craig et al. APPLICANT: VENTER, J. Craig et al. TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF THE PERFERENCE. CLOOTION	US-09-949-016-16785; Application US/09949016; Sequence 16785, Application US/09949016; Pattent No. 6812339;	Cy 648 ArgGINGLUAKGARGARGARGARGARGARGARGARGARGARGARGARGARG	629 MetGlyGlyArgArgGlyGlyArgGly 1599	609 GlyPheGlyGlyGlyArgArgGlyGlyProGlyGlyProDroGlyProLeumecGluGin 6	1533 CGGGGCGCGGGGACCGTGGAGGCTTCCGAGGGGGCCGGGGTGGGGACAGAGGT

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Qy 430PheAspGlyLysAspPheGlnGlySerLysLeuLysValSerLeuAlaArgLy 447	<u> 5</u> ⋅ 8
Qy 422 Thràlalysalalavalglu-Trp	<u> </u>
Qy 402 LeuAspLysGluThrGlyLysFroLysGlyAspAlaThrValSerTyrGluAspProFro 421 ::: ::: Db 31405 TTAGAGAAGTTACAGGCAGACCTAATGCATCTGGGAGTGG-TCATTTGATGATGATGAT 31460	<u> </u>
US-10-791-017A-2 (1-656) x US-09-949-016-16785 (1-35784)	g
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Patent No. 6812339 GENERAL INFORMATION: APPLICANT: VENTER, J. Craig et al. APPLICANT: VENTER, J. Craig et al. TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES FILE REFERENCE: CL001307	32764 528 32824	32705 CTGGTTAGGGACACTAGTCAGCCATTCACTGGACGCTTCAGAGCCTTCTGAAGATTGATT
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Qy 553 oProProPheProProPro	472 31985	47231926 CAGTGGCTCACGCCTGTAATCCCCAGCACTTTGGGAGGCTGAGGTGGGCGGATCACCTGAG
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32825	31805	31746 AGTCAATACTAGACTATCGAGAGCTAACAATGAATGTTTGTT
Qy 528		

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APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
ATTLE OF INVENTION: Expressed Sequence Tags a
Fatent No. 6783961
FILE REFERENCE: 59.USZ.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILLING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
           Percent Similarity:
Best Local Similarity:
Query Match:
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; Sequence 1657, Application US/09513999C
; Patent No. 6783961
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SEQ ID NO 1657
LENGTH: 454
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ORGANISM: Homo sapiens
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Sequence 13361, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
ITILE OF INVENTION: ESTs and Encoded Human P
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: PATENT. DATE
SEQ ID NO 13361
LENGTH: 411
TYPE: DNA
DECANTON.
                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens US-09-621-976-13361
                                                                                                                                                                                                                                                          US-10-791-017A-2 (1-656) x US-09-621-976-13361 (1-411)
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                      378.AlaAspPheDheLysGlnCysGlyValValLysMetAsnLysArgThrGlyGlnProMet
                                                                                                      358 SerAspAsnSerAlaIleTyrValGlnGlyLeuAsnAspSerValThrLeuAspAspLeu
                                                                                                                                                                                                               338 GlyProMetAspGluGlyProAspLeuAspLeuGlyProProValAspProAspGluAsp
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                                                                                                                                                                       62 GGACCCATGGATGAAGGACCAGATCTTGATCTAGGCCCACCTGTAGATCCAGATGAAGAC
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  GCAGACTTCTTTAAGCAGTGTGGGGTTGTTAAGATGAACAAGAGAACTGGGCAACCCATG
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99.15%
99.15%
16.76%
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Matches:
Conservative:
Mismatches:
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-08
NUMBER OF SEG ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity:
Query Match:
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US-09-949-016-66382
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US-09-949-016-66382/c
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   US-09-220-132-82
                  RESULT 13
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                                                                   ThrThrAlaThrValThrThrThrGlnAlaSerTyrAla 113
                                                                                                                                   ThralaProGlnAlaTyrSerGlnProValGlnGlyTyrGlyThrGlyAlaTyrAspThr
                                                                                                                                                                             TATGGGCAGACCGCCTATGCAACTTCTTATGGACAGCCTCCCACTGGTTATACTACTCCA
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GENERAL INFORMATION:

APPLICANT: Shyjan, Andrew W.

TITLE OF INVENTION: METHODS AND COMPOSITONS FOR THE IDENTIFICATION AND ASSESSMENT
TITLE OF INVENTION: OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CAN
FILE REFERENCE: 07334-074001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: I
SEQ ID NO 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 82, Application US/09220132
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CURRENT FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: US 60/079,303
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: US 60/068,821
PRIOR FILING DATE: 1997-12-24
NUMBER OF SEQ ID NOS: 191
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TYPE: DNA
ORGANISM: Homo sapiens
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ThrGlnProThrSerTyrAspGlnSerSerTyrSerGlnGlnAsnThrTyrGlyGlnPro
                                                                                                                                                                                                                                                               TyrGlyThrGlnProAlaTyrProAlaTyrGlyGlnGlnProAlaAlaThrAlaProThr 137
                                                                                                                                                                                                                                                                                                                                                                                               ThrProThrAlaProGlnAlaTyrSerGlnProValGlnGlyTyrGly---ThrGlyAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ThrTyrGlyGlnThrAlaTyrAlaThrSerTyrGlyGlnProPro---ThrGlyTyrThr 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TACCCCACCCAGCCGGGCAGGGCTATTCCCAGCAGAGCAGTCAGCCCTACGGACAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FastSEQ for Windows Version
                                                                                                                                           TyrAsnGlnProSerLeuGlyTyrGlyGlnSerAsnTyrSerTyrProGlnValProGly
                                                                                                                                                                                                          ArgProGlnAspGlyAsnLysProThrGluThrSerGlnProGlnSerSerThrGlyGly 157
                                                                                                                                                                                                                                             TATGGC-----AGTAGCCAGAGCTCCCAATCGTCT
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                                                                                                                                                                                                                                                                                                                                                                          ACTCAGTCAACTCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGGCCTCAAACGATTATACC-----CAACAAGCAAGCCAAAGCTATGGGGCC
                                                                               SerTyrProMetGlnProValThrAlaProProSerTyrProProThrSerTyrSerSer 197
                                                                                                               TACGGTAGCAGTTCT-----CAGAGCAGCAGCTATGGGCAGCCCCAG---AGTGGG
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486.00
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Matches:
Conservative:
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                                             ----GlyAsnValGlnHisArgAlaGlyAspTrp
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237 ProThrSerTyrProProGlnThrGlySerTyrSerGlnAlaProSerGlnTyrSerGln

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                            Alignment Scores:
US-10-791-017A-2 (1-656) x US-08-343-443B-106 (1-954)
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ATTORNEY/AGENT INFORMATION:
NAME: Welser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 989.0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEPAX: 215-875-8394
INFORMATION FOR SEQ ID NO: 106:
SEQUENCE CHARACTERISTICS:
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Patent No. 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 19102

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: AEDIT 1.0 DOS text edit.

CURRENT APPLICATION DATA:
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TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                            FEATURE:
NAME/KEY:
LOCATION:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/
FILING DATE: 19-MAY-1993
PRIOR APPLICATION DATA:
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ADDRESSEE: Weiser & Associates
STREET: 230 South Fifteenth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER
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                                                                                                               No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/0 FILING DATE: 18-NOV-1994 CLASSIFICATION: 514
                                                                                                                                                                                                                                               TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
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Desmaze, Chantal
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Ploougastel, B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCT/FR93/00494
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Qy 98 TyrAspThrThrAlaThrValThrThrGlnAlaSerTyrAlaAlaGlnSerAla 117	79 ThrProThrAlaProGlnAlaTyrSerGlnProValGlnGlyTyrGlyThrGlyAla 9	60 ThrTyrGlyGlnThrAlaTyrAlaThrSerTyrGlyGlnProProThrGlyTyrThr 7	40 SerTyrGlyThrTyrGlyGlnProThrAspValSerTyrThrGlnAlaGlnThrThrAla 	TyrThrAlaGlnProThrGlnGlyTyrAlaGlnThrThrGlnAlaTyrGlyGlnGln	Qy 1 MetAlaSerThrAspTyrSerThrTyrSerGlnAlaAlaAlaGlnGlnGlyTyrSerAla 20	13.32% Indels: 4 Gaps: 6) x US-09-919-039-323 (1-1684)	Pred. No.: 1.21e-17 Length: 1684 Score: 484.00 Autches: 177 Percent Similarity: 40.688 Conservative: 61 Best Local Similarity: 30.268 Mismatches: 173	; OTHER INFORMATION: Incyte ID No. 6727066 1813444CB1 US-09-919-039-323 Alignment Scores:		; NUMBER OF SEQ ID NOS: 401 ; SOFTWARE: PERL Program ; SEQ ID NO 323 Program ; LENGTH: 1684			RESULT 15 US-09-919-039-323 ; Sequence 323, Application US/09919039 ; Patent No. 6727066	Qy 317 ArgGlyGlyArgGlyMetGly 325	OY 297 ProAspAsnArgGlyArgGlyArgGlyGlyFheAspArgGlyGlyMetSerArgGlyGly 316	OY 277 ValTyrGlyGlnGluSerGlyGlyPheSerGlyProGlyGluAsnArgSerMetSerGly 296	Qy 257 GlnSerSerSerTyrGlyGlnGlnSerSerPheArgGlnAspHisProSerSerMetGly 276
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440 uLysValSerLeuAlaArgLysLysProProMetAsnSerMetArgGlyGlyLeuProPr 460	420 oProThrAlaLysAlaAlaValGluTrpPheAspGlyLysAspPheGlnGlySerLysLe 440	400 eTyrLeuAspLysGluThrGlyLysProLysGlyAspAlaThrValSerTyrGluAspPr 420	381 Phe-LysGlnCysGlyValValLysMetAsnLysArgThrGlyGlnProMetIleHisIl 400 ::: ::	361 SerAlaIleTyrValGlnGlyLeuAsnAspSerValThrLeuAspAspLeuAlaAspPhe 380 ::: ::: 948 GCAGCTGAGTCATTGCCTTTCTCCTTCGGGACACTGTCCAGCTGGGAGCTGGAAGCCTGG 1007	343GIYETGABPLEUGABPLEUGLYETGETGVALASPETGABPGLUASPSETASPASH 360 888 CATACATCACCACACCTGAAAGCAGATGTGCTTTTCCAGACTGATCCAACTGCAGAGAGTG 947	326 SeralaGlyGluArgGlyGlyPheAsnLysProGlyGlyProMetAspGlu 342 831 GGAAGTGACCGTGGTGGCTCAATAAATTTGGTGTGTTCAAGAAGAAGTGTATCTT 887	306 GlyPheAspArgGlyGlyMetSerArgGlyGlyArgGlyGlyArgGlyGlyMetGly 325	286 SerGlyProGlyGluAsnArgSerMetSerGlyProAspAsnArgGlyArgGlyArgGly 305	266 SerPheArgGlnAspHisProSerSerMetGlyValTyrGlyGlnGluSerGlyGlyPhe 285 ::: 702 CGTGGACGCCGCGCACGGGTGGCAGTGGTGGC	246 SerTyrSerGlnAlaProSerGlnTyrSerGlnGlnSerSerSerTyrGlyGlnGlnSer 265	231SerTyrGlyGlnGlnProProThrSerTyrProProGlnThrGly 245	218 SerSerTyrGlyGlnGlnSerSerTyrGlyGlnGlnSer	198 ThrGlnProThrSerTyrAspGlnSerSerTyrSerGlnGlnAsnThrTyrGlyGlnPro 217	178 SerTyrProMetGlnProValThrAlaProProSerTyrProProThrSerTyrSerSer 197 450 AGCTACAGCCAGCAGCCT	158 TyrasnGlnProSerLeuGlyTyrGlyGlnSerAsnTyrSerTyrProGlnValProGly 177	138 ArgProGlnAspGlyAsnLysProThrGluThrSerGlnProGlnSerSerThrGlyGly 157	, 118 TyrGlyThrGlnProAlaTyrProAlaTyrGlyGlnGlnProAlaAlaThrAlaProThr 137

Db Sear Job	유 성	<u> </u>	B 8	용 <i>성</i>	용 왕
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CY 518 GALGLYASDITP 522 DE 111 STECCCCACTTGG 1483 Db 1471 GTCCCCCACTTGG 1483 Search completed: February 21, 2005, 04:22:17 Job time : 451.042 secs	509ProSerGlyGly	494ArgGlyGlyPheProProArgGlyProArgGlySerArgGlyAsn 508	484 tGlyargmetGlyGlyargGlyGlyasp	480ProGlyGlyProMe 484 1237 ACCAAGGGAGAACCAGGAAACAGAGTGGTCATTCCCCAGCCCGGGCTGGAAAGC 1296	460 oArgGluGlyArgGlyMetProProProLeuArgGlyGlyProGlyGlyProGlyGly 479

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-THR_MIN=0 -ALIGN=15 -WODE=LOCAL -OUTFMT=ptto -NORM=ext -HEAPSIZE=500 -MINLEN=0
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Listing first 45 summaries
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Fgapop 6.0 , 1
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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

US-09-880-107-3769

Sequence 3769, Application US/09880107 Patent No. US20020142981A1 GENERAL INFORMATION:

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APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Joseph G.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
FRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR PILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: Patentin Ver. 2.1
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Pred. No.:
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TYPE: DNA
ORGANISM: Homo sapiens
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Qy 41 TyrGlyThrTyrGlyGlnProThrAspValSerTyrThrGlnAlaGlnThrThrAlaThr 60	TTACAGTACCTATAGCCAAGCTGCAGCACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	US-10-791-017A-2 (1-656) x US-09-873-319-717 (1-2390) Qy	Mismatches: Indels: Gaps:	Percent Similarity: 100.00% Conservative: 0	HER INF 873-319	LENGTH: 2390 LENGTH: 2390 TYPE: DNA ORGANISM: Homo sapiens PERTURE: A CONTROL OF CON	EARLIER FILING DATE: 2000-08-07 NUMBER OF SEQ ID NOS: 755 SOPTWARE: Patentin Ver. 2.1 SED ID NO 717		APPLICANT: Waga, Iwao APPLICANT: Waga, Iwao APPLICANT: Yamamoto, Jun APPLICANT: Yamamoto, Jun TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic TITLE OF INVENTION: Hyperplatia Heing Gene Expression Profiles	GENERAL INFORMATION: APPLICANT: Munger, William E. APPLICANT: Kulkarni, Prakash APPLICANT: Kulkarni, Prakash APPLICANT: Kulkarni, Prakash	RESULT 3 US-09-873-319-717 Sequence 717, Application US/09873319A Publication No. US2003011432481	Qy 641 LysMetAspLysGlyGluHisArgGlnGluArgArgAspArgProTyr 656 	Qy 621 ProProGlyProLeuMetGluGlnMetGlyGlyArgArgGlyGlyArgGlyGlyProGly 640	Qy 601 GlyGlyArgGlyMetAspArgGlyGlyPheGlyGlyGlyArgArgGlyGlyProGlyGly 620	Qy 581 ArgGlyGlyProGlyGlyMetPheArgGlyGlyArgGlyGlyAspArgGlyGlyPheArg 600	Qy 561 GlyaspargGlyargGlyGlyProGlyGlyMetArgGlyGlyArgGlyGlyLeumetAsp 580	Qy 541 AsnGlnCysLysAlaProLysProGluGlyPhaLeuProProProPheProProBroGly 560
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TYPE: DNA

ORCANISM: Homo sapie
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Publication No. US20040197827A1
GENERAL INFORMATION:
APPLICANT: JENAPHARM GmbH & Co. KG
TITLE OF INVENTION: Methods for Determining Hormonal Effects of Substances
FILE REFERENCE: Pat 3684/11
CURRENT APPLICATION NUMBER: US/10/791,017A
CURRENT FILING DATE: 2004-03-02
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 2390
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                                                       GlyArgGlyArgGlyGlyPheAspArgGlyGlyMetSerArgGlyGlyArgGlyGlyGly
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RESULT 5
US-09-822-830A-49/c
; Sequence 49, Application US/09822830A
; Patent No. US20020142952A1
; GENERAL INFORMATION:
; APPLICANT: Genetics Institute, Inc.
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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APPLICANT: Agostino, Michael J.
APPLICANT: Howes, Steven H.
APPLICANT: Howes, Steven H.
APPLICANT: Resnick, Richard J.
APPLICANT: Gulukota, Kamalakar
APPLICANT: Gulukota, Kamalakar
ITILE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SEC
FILE REFERENCE: GIN 6402
CURRENT APPLICATION NUMBER: US/09/822,830A
CURRENT FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/195,604
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 631
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 49
LINGTH: 2176
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-830A-49
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ACTAGTTATGATCAGAGCAGTTACTCTCAGCAGAACACCTATGGGCAACCGAGCAGCTAT
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Patent No. US20020142952A1

GENERAL INFORMATION:

APPLICANT: Wong, Gordon G.

APPLICANT: Wong, Gordon G.

APPLICANT: Wong, Gordon G.

APPLICANT: Howes, Kim

APPLICANT: Agostino, Michael J.

APPLICANT: Resnick, Richard J.

APPLICANT: Gulukota, Kamalakar

APPLICANT: Gruhkota, Kam
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APPLICANT: ISHII, SHIZUKO APPLICANT: YAMAMOTO, JUN-ICHI APPLICANT: ISONO, YUUKO APPLICANT: HIO, YURI APPLICANT: OTSUKA, KAORU APPLICANT: IRLE, RYOTARO APPLICANT: TAMECHIKA, ICHIRO APPLICANT: TAMECHIKA, ICHIRO APPLICANT: OTSUKA, KOTOYUKI APPLICANT: NAGALARI, KENNI APPLICANT: NAGHARI, KOTOYUKI APPLICANT: NASUHO, YASUHIKO TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA FILE REFERENCE: 084335/0160 CURRENT APPLICATION NUMBER: US/10/094,749 CURRENT FILING DATE: 2002-03-12 PRIOR APPLICATION NUMBER: 60/350,435 PRIOR FILING DATE: 2001-09-14 NUMBER OF SEQ ID NOS: 3381 SOFTWARE: Patentin Ver. 2.1	Db 397 ATGGATAAAGGCGAGCACCGTCAGGAGCGCAGAGATCGGCCCTAC 353 RESULT 7 US-10-094-749-1074 ; Sequence 1074, Application US/10094749 ; Publication No. US20030219741A1 ; GENERAL INFORMATION: ; APPLICANT: ISCGAI, TAKAO ; APPLICANT: SUGIYAMA, TOMOYASU ; APPLICANT: OTSUKI, TETSUJI ; APPLICANT: WAKAMATSU, AI ; APPLICANT: SATO, HIROYUKI	Db 637 GATCGTGGCAGAGGTGGCCTGGTGGCATGGGAGGAAGAGGTGGCCTCATGGATCGT 578 Gy 582 GlyGlyProGlyGlyMetPheArgGlyGlyArgGlyGlyAepArgGlyGlyPheArgGly 601 Db 577 GGTGGTCCCGGTGGATGTTCAGAGGTGGCCGTGGTGGAGAAGAAGGTGGCTTCCGTGGT 518 Gy 602 GlyArgGlyMetAspArgGlyGlyPheGlyGlyGlyArgArgArgGlyGlyProGlyGlyPro 621 Db 517 GGCGGGGCATGGACCGAGGTGGCTTCGTGGTGAGAAGACGAGGTGGCTTCCGTGGT 518 Gy 602 GlyArgGlyMetAspArgGlyGlyPheGlyGlyArgArgArgGlyGlyProGlyGlyPro 621 Db 517 GGCCGGGGCATGGACCGAGGTTGGTTTTGTGAGGAAGACGAGGTGGCCCTGGGGGCCC 458 Gy 622 ProGlyProLeuMetGluGlnMetGlyGlyArgArgArgArgArgGTyGlyProGlyLy8 641 Db 457 CCTGGACCTTTGATGGAACAGATGGGAAGAAGAGGAGGACCTGGAAAA 398 Gy 642 MetAspLyGGlyGluHisargGlnGluArgArgArgArgArgArgArgArgArgArgArgArgArgA	462 GluGlyArgGlyMetProProLeuArgGlyGlyProGlyGlyProBroCragGagGCCCAGGAGGTCCTGGG 482 GlyProMetGlyArgMetGlyGlyArgGlyGlyAspArgGlyGlyProBroProArgGly 826 GGACCCATGGGTCGCATGGGAGGCCGTGGAGGAGATAGAGGAGGCTTCCCTCCAAGAGGA 502 ProArgGlySerArgGlyAspProSerGlyGlyGlyAsnValGlnHisArgAlaGlyAsp

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APPLICANT: O'Connell, Peter
APPLICANT: O'Connell, Peter
TITLE OF INVENTION: Differential Patterns of Gene Expression that Predict for Docetax
TITLE OF INVENTION: Chemosensitly and Chemoresistance
TITLE OF INVENTION: Docetax
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Publication No. US20040018527A1
GENERAL INFORMATION:
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	Qy 60 ThrTyrGlyGlnThrAlaTyrAlaThrSerTyrGlyGlnProProThrGlyTyrThrThr 79 ::::: :::	Qy 40 SerTyrGlyThrTyrGlyGlnProThrAspValSerTyrThrGlnAlaGlnThrThrAla 59	Qy 21 TyrThrAlaGlnProThrGlnGlyTyrAlaGlnThrThrGlnAlaTyrGlyGlnGln 39	Qy 1 MetAlaSerThrAspTyrSerThrTyrSerGlnAlaAlaAlaGlnGlnGlyTyrSerAla 20:	/ Match: 35.27% Indels: Gaps: 0-791-017A-2 (1-656) x US-10-755-889-649 (1-1822)) ORGANISM: Homo sapiens US-10-755-889-649 Alignment Scores:	; SOFTWARE: PatentIn version 3.2 ; SEQ ID NO 649 ; LENGTH: 1822 ; TYPE: DNA	PRIOR FILING DATE: 2003-05-12 NUMBER OF SEQ ID NOS: 823	; FILE REFERENCE: DO284 NP; CURRENT APPLICATION NUMBER: US/10/755,889; CURRENT FILING DATE: 2004-01-13; PRIOR APPLICATION NUMBER: U.S. 60/440,068	, GENERAL INFORMATION: APPLICANT: Bristol-Myers Squibb Company TITLE OF INVENTION: PATHWAY TITLE OF INVENTION: PATHWAY	RESULT 9 US-10-755-889-649 / Sequence 649, Application US/10755889 / Publication No. US20040171823A1	Qy 648 ArgGlnGluArgArgArgProTyr 656	Qy 629 MetGlyGlyArgArgGlyGlyArgGlyGlyFroGlyLysMetAspLysGlyGluHis 647			₃ —<	Qy 573 GlyGlyArgGlyGlyLeuMetAspArgGlyGlyProGlyGlyMetPheArgGly 590	
. Q	B &) B 4	S B 8	, p. 5	р , Q	B &	B &	B &	B &) B 24	, B 8	B Q	g Q	dg Qy	D 4	\$ E	\$ 5	용 성	gg VQ
435 PheGlnGlySerLysLeuLysValSerLeuAlaArgLysLysProProMetAsnSerMet 454	415 VALSETTYKGLUABPPTOPTOTNIALALYBALBALAVALGUUTTPPNEASPGLYLYBASP 434 ::::: ::: GTCTCTTTTGATGACCCACCTTCAGCTAAAGCAGCTATTGACTGGTTTGATGGTAAAGAA 1143		375 ASDABDLEUN.LAABDPHEPHELYSGLINCYSGLYVALVALLYSMECKABILYSKIGTINGGLY 394 395 SILLYSMECKABILYSKIGTINGGLYSKIGTIN		335 LysProGlyGlyProMetAspGluGlyProAspLeuAspLeuGlyProProValAspPro 354	317 ArgGlyGlyArgGlyGlyMetGlySerAlaGlyGluArgGlyGlyPheAsn 334	299 AsnargGlyArgGlyArgGlyPheAspArgGlyGlyMetSerArgGlyGly 316	279 GlyGlnGluSerGlyGlyPheSerGlyProGlyGluAsnArgSerMetSerGlyProAsp 298	634 GGCAGTGGTGGCGGTTATGGCAATCAAGACCAGAGTGGTGGAGGTGGCAGCGGTGGCTAT 693	239 SerTyrProProGlnThrGlySerTyrSerGlnAlaProSerGlnTyrSerGlnGlnSer 258	219 SerTyrGlyGlnGlnSerSerTyrGlyGlnGlnSerSerTyrGlyGlnGlnProProThr 238	199 GlnProThrSerTyrAspGlnSerSerTyrSerGlnGlnAsnThrTyrGlyGlnProSer 218	179 TyrProMetGlnProValThrAlaProProSerTyrProProThrSerTyrSerSerThr 198	159 AsnGlnProSerLeuGlyTyrGlyGlnSerAsnTyrSerTyrProGlnValProGlySer 178	385CCCAGCAGCACCTCGGGAAGTTAC 408	343 GGGCAGCAGTICTICTATICTIGGCTATIGGCCAGCAGCCAGCTAGTICTAGTICTICTICTAGTICT	119 GlyThrGlnProAlaTyrProAlaTyrGlyGlnGlnProAlaAlaThrAlaProThrArg 138	99 ABpThrThrAlaThrValThrThrThrGlnAlaSerTyrAlaAlaGlnSerAlaTyr 118 ::: :::: ::: 313 GGCAGTAGCCAGAGCTCCCAATCGTCTTAC 342	80 ProThrAlaProGlnAlaTyrSerGlnProValGlnGlyTyrGlyThrGlyAlaTyr 98

Alignment Scores: 6.61e-83 Length: 1939 Pred. No.: 6.61e-83 Length: 301 Score: 1273.50 Matches: 301	; NAME/KEY: m18C reature ; OTHER INFORMATION: Incyte ID No. US20030108871A1 478620.53 US-09-919-039-322	Homo	; CURRENT FILING DATE: 2002-09-09; PRIOR APPLICATION NUMBER: 60/222,113; PRIOR FILING DATE: 2000-07-28; NUMBER OF SEQ ID NOS: 401	APPLICATION NO	; GENERAL INFORMATION: ; APPLICANT: Kaser, Matthew R. ; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES	RESULT 10 US-09-919-039-322 ; Sequence 322, Application US/09919039 ; Publication No. US20030108871A1	Db 1624 CAGGATCGCAGGGAGAGGCCGTAT 1647	Qy 649 GlnGluArgArgArgProTyr 656	Qy 630 GlyGlyArgArgGlyGlyArgGlyGlyFroGlyLy8MetAspLy8GlyGluHisArg 648	Db 1585 TTT 1587	1525 GGCCGCGGGGACCGTGAAGGCTTCCGAGGGGCCGGGGTGGTGGGGACAGAGGTGGC	Qy 591 GlyArgGlyGlyAspArgGlyGlyPheArgGlyGlyArgGlyMetAspArgGlyGly 609	574 GlyArgGlyGlyLeuMetAspArgGlyGlyProGlyGlyMetPheArgGly	Qy 555 ProPheProProGlyGlyAspArgGlyArgGlyGlyProGlyGlyMetArgGly 573	Qy 535 AlaTzpArgThrGluCysAsnGlnCysLysAlaProLysProGluGlyPheLeuProPro 554	Qy 515 ValGlnHisArgAlaGlyAspTrpGlnCysProAspProGlyCysGlyAsnGlnAsnPhe 534	Qy 495 GlyGlyPheProArgGlyProArgGlySerArgGlyAsnProSerGlyGlyGlyAsn 514	Qy 475 GlyGlyProGlyGlyProGlyGlyProMetGlyArgMetGlyGlyArgArgArg 494	1198	::: ::: ::::::
Oy 316 GlyArgGlyGlyArgGlyGlyMetGlySerAlaGlyGluArgGlyGlyPhe 333	Qy 298 AspAsnArgGlyArgGlyArgGlyGlyPheAspArgGlyGlyMetSerArgGly 315	Qy 278 TyrGlyGlnGluSerGlyGlyPheSerGlyProGlyGluAsnArgSerMetSerGlyPro 297	Db 594 GGAGGTGGAGGTAACTATGGCCAAGATCAATCCTCCATGAGTAGTGGT 641 Qy 258 SerSerSyrGlyGlnGlnSerSerPheArgGlnAspHisProSerSerMetGlyVal 277	Qy 238 ThrSerTyrProProGlnThrGlySerTyrSerGlnAlaProSerGlnTyrSerGlnGln 257	Qy 218 SerSerTyrGlyGlnGlnSerSerTyrGlyGlnGlnFroPro 237 ::: Db 535 CAGGGCTATGGACAGAACCAGTACAACAGCAGCAGTGGTGGAGAGGTGGAGAGTT- 593	Qy 198 ThrGlnProThrSerTyrAspGlnSerSerTyrSerGlnGlnAsnThrTyrGlyGlnPro 217		Qy 178 SerTyrProMetGinProValThrAlaProProSerTyrProProThrSerTyrSerSer 197	Qy 158 TyrAsnGlnProSerLeuGlyTyrGlyGlnSerAsnTyrSerTyrProGlnValProGly 177	Db 394	4 - 4.1			Qy 79 ThrProThrAlaProGlnAlaTyrSerGlnProValGlnGlyTyrGlyThrGlyAla 97	Qy 60 ThrTyrGlyGlnThrAlaTyrAlaThrSerTyrGlyGlnProProThrGlyTyrThr 78	Qy 40 SerTyrGlyThrTyrGlyGlnProThrAspValSerTyrThrGlnAlaGlnThrThrAla 59	Oy 21 TyrThrAlaGlnProThrGlnGlyTyrAlaGlnThrThrGlnAlaTyrGlyGlnGln 39	Qy 1 MetAlaSerThrAspTyrSerThrTyrSerGlnAlaAlaAlaGlnGlnGlyTyrSerAla 20	US-10-791-017A-2 (1-656) x US-09-919-039-322 (1-1939)	Percent Similarity: 53.96% Conservative: 60 Best Local Similarity: 44.99% Mismatches: 153 Query Match: 35.05% Indels: 156 DB: 10 Gaps: 30

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RESULT 11
US-10-425-115-182496
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1632 AGACAGGATCGCAGGGAGAGGCCGTAT 1658
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APPLICANT: LA ROSA, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Cao, Yihua

APPLICANT: Cao, Yongwei

FITTLE OF INVENTION: Nucleic Acid Molecules and TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(53222)B

CURRENT FILLING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 182496

LENGTH: 763

TYPE: DNA

ORGANISM: Zea mays
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NAME/KEY: unsure
LOCATION: (1)..(763)
OTHER INFORMATION: unsure at all n locations
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OTHER INFORMATION: Clone ID: MRT4577_98018C.1
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                                                                        ProSerLeuGlyTyrGlyGlnSerAsnTyrSerTyrProGlnValProGlySerTyrPro
                                                                                                                                  AspGlyAsnLysProThrGluThrSerGlnProGlnSerSerThrGlyGlyTyrAsnGln
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                                                                                                                   GATGGTAACAAGCCTGCTGAGACTAGTCAACCTCAATCTAGCACAGGGGGTTATAACCAA
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   ATGCAGCCAGTCACCGCACCTCCATCTTATCCTCCTACCAGCTACTCCTCTTCACAGCCG
                                                         CCCAGCCTAGGATATGGACAGAGTAACTACAGCTATCCCCAGGTACCTGGGAGCTACCCA
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9847
LENGTH: 2299
TYPE: DNA
COGNAUSM: Homo sapiens
US-10-198-846-9847
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APPLICANT: Lillie, James
APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzhen
APPLICANT: Wang, Youzhen
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: FOVEL GENES, COMPOSITIONS, KITS,
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT,
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
FILE REFERENCE: MRI-049
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CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
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                                                 LeuProProArgGluGlyArgGlyMetProProProLeuArgGlyGlyProGlyGlyPro
                                                                                                   SerLysLeuLysValSerLeuAlaArgLysLysProProMetAsnSerMetArgGlyGly
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Conservative:
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US-10-791-017A-2 (1-656) x US-09-918-995-27690 (1-550)
                                                                                    Score:
                                                                                                  Pred. No.:
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Sequence 27690, Application US/09918995

| Publication No. US20030073623A1
| GENERAL INFORMATION:
| APPLICANT: Hyseq, Inc.
| TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBT TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES FILE REFERENCE: 20411-756
| CURRENT APPLICATION NUMBER: US/09/918,995
| CURRENT FILING DATE: 2001-07-30
| PRIOR APPLICATION NUMBER: US/09/235,076
| PRIOR FILING DATE: 1999-01-20
| NUMBER OF SEQ ID NOS: 38054
| SOFTWARE: FastSEQ for Windows Version 3.0
| SEQ ID NO 27690
| LENGTH: 550
| TYPE: DNA | Homo sapiens | FastTup.
                                                                                                                                                      ; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)... (550)
; OTHER INFORMATION: n = A
US-09-918-995-27690
                Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-918-995-27690
                                                                                                                   Alignment Scores:
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7.63e-61
961.00
97.65%
97.65%
26.45%
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                Length:
Matches:
Conservative:
Mismatches:
Indels:
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; TYPE: DNA
; OTGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1) ... (568)
; OTHER INFORMATION: n = A
US-09-918-995-9557
                                                                                                                                                                                                                                                                                                                                Sequence 9557, Application US/09918995

Publication No. US20030073623A1

GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OF TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES FILE REFERENCE: 20411-756

CURRENT APPLICATION NUMBER: US/09/918,995

CURRENT PILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US/09/235,076

PRIOR FILING DATE: 1999-01-20

NUMBER OF SEQ ID NOS: 38054
                                                             Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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US-09-918-995-9557
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                              US-10-791-017A-2 (1-656) x US-09-918-995-9557 (1-568)
                                                                                                                        Score:
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                                                                                                                                        Pred. No.:
                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 9557
LENGTH: 568
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                                                            3.74e-54
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97.08%
97.08%
23.91%
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Matches:
Conservative:
Mismatches:
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
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US-09-864-761-8001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8001, Application US/09864761 Patent No. US20020048763A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY FILE REFERENCE: Acomica-X-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173
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FOR

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TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

PEATURE:

OTHER INFORMATION: MAP TO AC018774.3

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.1

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.4

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.4

OTHER INFORMATION: EXPRESSED IN FORMATION; SIGNAL = 3.4

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.1

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.4

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.9

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6
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Best Local Similarity:
Query Match:
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2000-06-30
PRIOR PILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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                                                                          141 AspGlyAsnLysProThrGluThrSerGlnProGlnSerSerThrGlyGlyTyrAsnGln
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42 ATGGCATCCATGGATTACAGTACCTATAGCCAAGCTGCAGCGCAGCAGCAGGGCTACAGTGCT
ProSerLeuGlyTyrGly 166
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95.18%
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Matches:
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Search completed: February 21, 2005, Job time : 3670.78 secs 08:39:34

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-MODELL-frame+_D2n.model -DEV-x1p
-Q-/cgn2_1/USPTO_spool_D/US10791017/runat_17022005_125807_22086/app_query.fasta_1.1358
-Q-/cgn2_1/USPTO_spool_D/US10791017/runat_17022005_125807_22086/app_query.fasta_1.1358
-DB=EST -QFMT=fastap -SUFFIX-p2n.rst -MINMATCH-0.1 -LOOPCIL-0 -LOOPEXT-0
-UNITS-bits -START=1 -END=-1 -MATRIX-blosum62 -TRANS-human40.dd1 -LIST=45
-DCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE-LOCAL
-OUTFMT=pto -NORM-ext -HEAPSIZE-500 -MINLEN=0 -MAXLEN=2000000000
-USER-US10791017 -QCGN_1 1_6628_grunat_17022005_125807_22086 -NCFU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPDP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
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3633
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                             Web: www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

Location/Qualifiers
                                                                                                                                                                                                                                     Unpublished Contact: Feng Liang Email: fliang@lifetech.com URL: Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2157)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Fill-length cDNA libraries and normalization
                                                                                                                                               Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                              Faraday Avenue
2 (bases 1 to 2157)
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HTC; CNSLT_cDNA.
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/clone="CSODIO10Y112"
/tissue_type="placenta Cot 2
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                                           ProProGlyProLeumetGluGlnMetGlyGlyArgArgGlyGlyArgGlyGlyProGly
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                                                                 Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invityogen.
                                                                                                                                                                                                                                                                        Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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   GluSerGlyGlyPheSerGlyProGlyGluAsnArgSerMetSerGlyProAspAsnArg
                                                        TyrGlyGlnGlnSerSerPheArgGlnAspHisProSerSerMetGlyValTyrGlyGln
                                                                                                                         ProProGlnThrGlySerTyrSerGlnAlaProSerGlnTyrSerGlnGlnSerSerSer
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LysMetAspLysGlyGluH1sArgGlnGluArgArgAspArgProTyr 656
                                                                                      ProProGlyProLeuMetGluGlnMetGlyGlyArgArgGlyGlyArgGlyGlyProGly
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Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
                                                                                                                                                                                                                                                                                                                                                                             1 GATTACAGTACCTATAGCCAAGCTGCAGCGCCAGCAGGGCTACAGTGCTTACACCGCCCAG
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1 (bases 1 to 2103)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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HTC; CNSLT_CDNA.
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                                           GCATACAGCCAGCCTGTCCAGGGGTATGGCACTGGTGCTTATGATACCACCACTGCTACA
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSDI076Y021"
/tissue_type="placenta_Cot_25-normalized"
/plasmid="pCMVSPORT_6"
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                                                                                                                                                              GlyValValLysMetAsnLysArgThrGlyGlnProMetIleHisIleTyrLeuAspLys
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full-length cDNA clone CS
of Homo sapiens (human).
CR602561
CR602561.1 GI:50483368
HTC; CNSLT_CDNA.
                                                                                                                            Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invirogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Verte
Mammalia; Butheria; Primates; Catarrhini; Hon
1 (bases 1 to 2070)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ InVitroGen Corporation
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Homo sapiens
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/tissue_type="Placenta
/plasmid="pCMVSPORT_6"
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Q B Q B			Alignment So Pred. No.: Score: Sercent Simi Best Local & Query Match. DB:		FEATURES Bource	TITLE JOURNAL COMMENT	AUTHORS TITLE JOURNAL REMARK REFERENCE AUTHORS	KEYWORDS SOURCE ORGANISM REFERENCE	RESULT 6 CR594868 LOCUS DEFINITION ACCESSION VERSION
121 GGACAGCCCACTGATGTCAGCTATACCCAGGCTCAGACCACTGCAACCTATGGGCAGACC 180 65 AlaTyrAlaThrSerTyrGlyGlnProProThrGlyTyrThrThrProThrAlaProGln 84	ProThrGlnGlyTyrAlaGlnThrThrGlnAlaTyrGlyGlnGlnSerTyrGlyThrTyr	14868 (1-2093) rGlnAlaAlaGlnGlnGlyT rCCAAGCTGCAGCGCAGCAGGGCT	1.16e-210 Length: 2093 1.16e-210 Length: 2093 1.16e-210 Matches: 651 1.16e-210 Matches: 0 1.16e-210 1.16e-	/mol type="mRNA" /db xref="taxon:9606" /clone="CSUDI064YE15" /tissue type="Placenta /plasmid="pCMVSPORT_6"	end enriched, double-strand CDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. Location/Qualifiers 1. 2093 /organiem="Homo sanions"	Direct Submission Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr) 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime	Full-length cDNA libraries and normalization Unpublished Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Paraday Avenue 2 (bases 1 to 2093) Genoscome.	HTC; CNSIT_cDNA. Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2093)	CR594868 2093 bp mRNA linear HTC 21-JUL-2004 full-length cDNA clone CS0DI064YE15 of Placenta Cot 25-normalized CR594868 CR594868 1 GI:50475675
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425 AlaAlaValGluTrpDheAspGlyLygaAspPheGlnGlySerLygleuLygValSerLeu	385 GIYVALIANBACASALYSASGTÜRGLÄSIGINFROMETIEHISTIETYFLEUASPLYS 404 1138 GGGTTGTTAGATGAACAAGAACTGGGGCAACCCATGATCACACTCTACTGACAAG 119 405 GluthrGlyLysBroLysGlyAspAlaThrValSerTyrGluAspProProThrAlalys 424	18 GATCTTGATCTAGGCCCACCTGTAĞATCCAĞATGAAĞACTCTĞACAACAĞTĞCAATTTAT 65 ValGlnGlyLeuAsnAspSerValThrLeuAspAspLeuAlaAspPhePheLysGlnCys	GlySerAlaGlyGluArgGlyGlyPheAsnLysProGlyGlyProMetAspGluGlyPro	285 PheSerGlyProGlyGluAsnArgSerMetSerGlyProAspAsnArgGlyArgGlyArgGlyArg 304	721 GGATCCTACAGCCAAGCTCCAAGTCAATATAGCCAACAGAGCAGCAGCTACGGGCAGCAG 780 265 SerSerPheArgGlnAspHisProSerSerMetGlyValTyrGlyGlnGluSerGlyGly 284	225 SerTyrGlyGlnGlnSerSerTyrGlyGlnGlnProProThrSerTyrProProGlnThr 244	185 ThrALAPTOPTOSETTYTPTOPTOTHTSETTYTSETSETTHTTHETOTHTSETTYTABD 204	421 CCCACTGAGACTAGTCAACCTCAATCTAGCACAGGGGGTTACAACCAGCCCAGCCTAGGA 480 165 TyrGlyGlnSerAsnTyrSerTyrProGlnValProGlySerTyrProMetGlnHlllllllllllllllllllllllllllllllllll	301 GTCACCACCAGGCCTCCTATGCAGCTCAGTCTGCATATGGCACTCAGCCTGCTTAT 360 125 ProAlaTyrGlyGlnGlnProAlaAlaThrAlaProThrArgProGlnAspGlyAsnLys 144

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                                                                                                   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage: BP 191 91006 EVRY cedex - FRANCE (B-mail: seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a
                                                                                                                                                                                                                                                         Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue
                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2126)

Li,W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization
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 /organism="Homo sapiens"
/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                         ThrAlaProProSerTyrProProThrSerTyrSerSerThrGlnProThrSerTyrAsp
                                                                                                                                                                                                                                                                                                                                                                                                                           PheSerGlyProGlyGluAsnArgSerMetSerGlyProAspAsnArgGlyArgGlyArg
                                                                             SerSerPheArgGlnAspHisProSerSerMetGlyValTyrGlyGlnGluSerGlyGly
                                                                                                                        GGATCCTACAGCCAAGCTCCAAGTCAATATAGCCAACAGAGCAGCAGCTACGGGCAGCAG
                                                                                                                                                                                  SerTyrG1yG1nG1nSerSerTyrG1yG1nG1nProProThrSerTyrProProG1nThr
                                                                                                                                                                                                                                                                                                                                                                                  TyrGlyGlnSerAsnTyrSerTyrProGlnValProGlySerTyrProMetGlnProVal 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProAlaTyrGlyGlnGlnProAlaAlaThrAlaProThrArgProGlnAspGlyAsnLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTCACCACCACCCAGGCCTCCTATGCAGCTCAGTCTGCATATGGCACTCAGCCTGCTTAT
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                                                                                                                                                                                                                                                                                                       ACTGCACCTCCATCCTACCCTCCTACCAGCTATTCCTCTACACAGCCGACTAGTTATGAT
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 TTTTCCGGACCAGGAGAACCGGAGCATGAGTGGCCCTGATAACCGGGGCAGGGGAAGA
                                                            AGTTCATTCCGACAGGACCACCCCAGTAGCATGGGTGTTTATGGGCAGGAGTCTGGAGGA
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	isArgGlnGluArgArgAspArgProTyr 656 	645 GlyGluHiøArg
7	GluGlnMetGlyGlyArgArgGlyGlyArgGlyGlyFroGlyLy8MetA8pLy8 644 	25 LeuMet 58 TTGATG
•	G1YG1YPheG1YG1YA1YA1GA1ZG1YG1YP1OG1YG1YP1OF1OG1YP1O 624 	605 MetAspArgGly 1798 ATGGACCGAGGT
	PheArgGlyGlyArgGlyAepArgGlyGlyPheArgGlyGlyArgGly 604 	585 GlyGlyMetPhe 1738 GGTGGAATGTTC
	ArgGlyGlyProGlyGlyMetArgGlyGlyArgGlyGlyLeuMetAspArgGlyGlyPro 584 	565 ArgGlyGlyPro
	ProGluGlyPheLeuProProProProPheProProProGlyGlyAspArgGly 564	45 18
	roGlyCysGlyAsnGlnAsnPheAlaTrpArgThrGluCysAsnGlnCysLys 544 	525 ProAsnProGly 1558 CCCAATCCGGGT
•	nCys 5	98 TCCCGAG
	GlyArgMetGlyGlyArgGlyGlyAspArgGlyGlyPheProProArgGlyProArgGly 504 	38
•	ProLeuArgGlyGlyProGlyGlyProGlyGlyProMet 484 	465 GlyMetProProProProProProProProProProProProProP
•	roProMetAsnSerMetArgGlyGlyLeuProProArgGluGlyArg 464 	
•	PPheAspGlyLysaspPheGlnGlySerLysLeuLysValSerLeu 444 	425 AlaAlaValGluTrpPheAgg
•	ProLyBGlyAspAlaThrValSerTyrGluAspProProThrAlaLys 424 CCAAAGGCGATGCCACAGTGTCCTATGAAGACCCACTGCCACTGCCAAG 1257	405 GluThrGlyLysPr 1198 GAAACAGGAAAGCC
	rGlyGlnPrometIleHisIleTyrLeuae 	85 GlyValValLys
7	PASPLeuAlaAspPhePheLysG] 	65 Valg
•	YProProValAspProAspGluAspSerAspAsnSerAlaIleTyr 364 	45 AspL 18 GATC
7	laGlyGluArgGlyGlyPheAsnLysProGlyGlyProMetAspGluGlyPro 344 	25 GlySerA 61 GGCG
	rgGlyGlyMetSerArgGlyGlyArgGlyGlyArgGlyGlyMet 324 	305 GlyGlyPheAspAi 901 GGGGGATTTGATCG

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                                                                                                                                                                                                   Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

AL Nature 420, 53-573 (2002)

CE 6 (bases 1 to 2107)

CE 6 (bases 1 to 2107)

CE 7 Arakawa T. Bono, H. Carninci, P. Fukuda, S. Fukunishi, Y. Furuno, M. Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiracka, T., Kato, H., Kasukawa, T., Kato, H., Sato, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Sato, H., Sasito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Direct Submission
Submitted (18-AUG-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RICEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishih,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishina,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Pujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
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Functional annotation of a full-length mouse Nature 409, 685-690 (2001)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                      MetAlaSerThrAspTyrSerThrTyrSerGlnAlaAlaGlnGlnGlyTyrSerAla
                   TATEGAACCTATEGACAGCCTACTGATGTCAGCTATACTCAGGCTCAGACCACTGCCACC
                                         TyrGlyThrTyrGlyGlnProThrAspValSerTyrThrGlnAlaGlnThrThrAlaThr
                                                                                                                       TyrThrAlaGlnProThrGlnGlyTyrAlaGlnThrThrGlnAlaTyrGlyGlnGlnSer
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/clone="3830417B11"
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1 (bases 1 to 2073)

11,W.B., Gruber,C., Jessee,J. and Polayes,D.

Pull-length cDNA libraries and normalization

Unpublished

Contact: Peng Liang Email: fliang@lifetech.com URL:

http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
  18t
           Direct Submission
Submitted (20-4) Genoscope - Centre National de Sequencage :
BP 191 9106 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
Web : www.genoscope.cns.fr)
                                                        Genoscope.
                                                                Faraday Avenue
2 (bases 1 to 2073)
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HTC; CNSLT_cDNA.
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 SerSerSerTyrGlyGlnGlnSerSerPheArgGlnAspHisProSerSerMetGlyVal
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Percent Similarity:
Best Local Similarity:
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODIOLIYO05"
/tissue_type="Placenta Cot 25
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Direct Submission

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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full-length cDNA clone CS0DG004YL23
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Full-length cDNA libraries
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2083)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                           ThrThrProThrAlaProGlnAlaTyrSerGlnProValGlnGlyTyrGlyThrGlyAla
                                                                                                                                                                                                                                                                     TyrSerAlaTyrThrAlaGlnProThrGlnGlyTyrAlaGlnThrThrGlnAlaTyrGly
 TyrAspThrThrAlaThrValThrThrThrGlnAlaSerTyrAlaAlaGlnSerAla
                                                                                                                                                                                                                                                    TACAGTGCTTACACCGCCCAGCCCACTCAAGGATATGCACAGGACCACCCAGGCATATGGG
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/mol type="mRNA"
/db_xref="taxon:9606"
/clone="CSODG004YL23"
/tissue_type="B cells (Ramos cell line)"
/plasmid="pCMVSPORT_6"
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477	LeuProProArgGluGlyArgGlyMetProProProLeuArgGlyGlyPro	UI
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43 12	8 GluAspProProThrAlaLysAlaAlaValGluTrpPheAspGl 	0 1
41 12	8 IleHisIleTyrLeuAspLysGluThrGlyLysBroLysG 3 ATCCACATCTACCTGGACAAGGAAACAGGAAAGCCCAAAG	
397 114	8 AlaAspPhePheLyéGlnCy6GlyValValLy8MetA8nLy8ArgT 	37 108
377	SeraspasnSeralaIleTyrValGlnGlyLeuasnAspS 	102
357 102	GlyPrometAspGluGlyProAspLeuAspLeuGlyP	96 33
337 962	GlyGlyArgGlyGlyMetGlySerAlaGlyGluArgGlyGlyPheAsnLySPI 	31 90
317 902	AspasnargGlyargGlyargGlyGlyPheaspargGlyGlyMets 	8 2 4 9
297 842		27 78
27 78	A—se	258 723
257 722	8 ThrSerTyrProProGinThrGlySerTyrSerGlnAlaProSerGinTyrSerGlnGln 25 	66
237	8—8 —8	21 60
60:	ThrGlnPı	19 54
197	SerTyrP	17 48
17	TyrasnGlnProSerLeuGlyTyrGlyGlnSerAsnTyrSerTyrProGlnValPr 	15 42
42 I	ArgProGI	13 36
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Genome Res.
20499374
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Hazada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
                                                                                                                                                                                    Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2373 bp mRNA linear HTC 03-APR-2004 Mus musculus 12 days embryo embryonic body between diaphragm region and neck cDNA, RIKEN full-length enriched library, clone:9430031M11 product:Ewing sarcoma homolog, full insert sequence.

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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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18 (bases 1 to 2373)

18 (bases 1 to 2373)

18 Adachi, J., Alzawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hasagaki, T., Haraoka, T., Hiraoka, T., Hiraoka, T., Hayashida, K., Hayatsu, N., Hiraoka, T., Kogawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sogabe, Y., Tagawa, A., Thinagawa, A., Shiraki, T., Sogabe, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.
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Genome Res.
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Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoham Kanagawa 230-0045, Japan (B-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

CDNA library was prepared and sequenced in Mouse Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prepare mouse tissues.
Please visit our web site for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Group Phase I & II Team.
Analysis of the mouse transcriptome of 60,770 full-length cDNAs
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                                                                                                                                                                                                                              evidence: BLASTN, putative"
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/mol_type="mRNA"
/strain="C57BL/6J"
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svidence: BLASTN, 99%, match=2172)
                                                                                                                                                                                                                                                                                                     /clone_lib="RIKEN full-length
/dev_stage="12 days embryo"
                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="FANTOM_DB:9430031M11"
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Homo sapiens (human)
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Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :

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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and Ecor V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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                                                                                                GlnProAlaTyrProAlaTyrGlyGlnGlnProAlaAlaThrAlaProThrArgProGln
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             GATGGAAACCAGCCCACTGAGACTAGTCAACCTCAATCTAGCACAGGGGGTTACAACCAG
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/mol_type="mRNA"
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/clone="CSODJ013YN08"
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	480 1455	61 ArgGluGlyArgGlyMetProProPr 96 CGTGAGGGCAGAGGCATGCCACCACC	
	460 1395	441 LysValSerLeuAlaArgLysLysProProMetAsnSerMetArgGlyGlyLeuProPro	
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	360 1095	341 AspGluGlyProAspLeuAspLeuGlyProProValAspProAspGluAspSerAspAsn 	
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	320 978	301 GlyargGlyargGlyGlyPheAspargGlyGlyMetSerArgGlyGlyArgGlyGlyGlyGly	
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	280 858	261 TyrGlyGlnGlnSerSerPheArgGlnAepHisProSerSerMetGlyValTyrGlyGln 	
	260 798	241 ProProGlnThrGlySerTyrSerGlnAlaProSerGlnTyrSerGlnGlnSerSerSer	
	240 738	221 GlyGlnGlnSerSerTyrGlyGlnGlnSerSerTyrGlyGlnGlnBroProThrSerTyr 	
	220 678	201 ThrSerTyrAspGlnSerSerTyrSerGlnGlnAsnThrTyrGlyGlnProSerSerTyr 	
	200 618	181 MetGlnProValThrAlaProProSerTyrProProThrSerTyrSerSerThrGlnPro	
	180 558	161 ProSerLeuGlyTyrGlyGlnSerAsnTyrSerTyrProGlnValProGlySerTyrPro	

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Punctional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)	enome Exp ortium.		äë,	റയ്ട്	O.	20499374 11042159	ation and subtraction of cap-trapper-selected cDNAs will-length cDNA libraries for rapid discovery of n	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh.M., Kompo.H., Okazaki,Y., Muramatsu.M. and Havashizaki,Y.	10349636	High-efficiency full-length cDNA cloning High-Enzymol. 303, 19-44 (1999)	The state of the s	mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Rutheria: Rodentia: Sciurcomathi: Muridae: Murinae: Mus	musculus (house mo	full insert sequence. AK049743 AK040743 GI-26001614	AK049743 2269 bp mRNA linear HTC 03-APR-2004 Mus musculus 12 days embryo spinal cord cDNA, RIKEN full-length enriched library, clone:C530046A18 product:Ewing sarcoma homolog,	GAGATCGGC	41 LysMetAspLysGlyGluHisArgGlnGluArgArgAspArgProTyr 656)76 CC-CCA 1880	31 ProProGlyProLeuMetGluGlnMetGlyGlyArgArgGlyGlyArgGlyGlyProGly 640	816 GGTGGCCGGGGCATGGACCGAGGTGGCTTTGGTGGAGGAAGACGAGGTGGCCCTGGGGGG 1875	GlyGlyArgGlyMetAspArgGlyGlyGlyGlyGlyArgArgGlyGlyProGlyGly	.756 CGTGGTGGTCCCGGTGGAATGTTCAGAGGTGGCCGTGGTGGAGACAGAGGTGGCTTCCGT 1815	81 ArgGlyGlyProGlyGlyMetPheArgGlyGlyArgGlyGlyAspArgGlyGlyPheArg 600	GTGATCGTGGCAGAGGTGGCCCTGGTGGCATGCGGGGAGGAAGAAGAGTGGCCTCATGGAT 1	GlvAanArqGlvArqGlvGlvProGlvGlvMetArqGlvGlvArqGlvGlvLeuMetAsp	AACCAGTGTAAGGCCCCAAAGCCTGAAGGCTTCCTCCCGCCACCCTTTCCGCCCCCGGGT 1	

Qy 1 MetalaSerThrAspTyrSerThrTyrSerGlnAlaAlaGlnGlnGlyTyrSerAla 20	Pred. No.: 1.74e-193 Length: 2269 Score: 3321.00 Hatches: 606 Percent Similarity: 93.45% Conservative: 7 Best Local Similarity: 92.38% Mismatches: 5 Query Match: 91.41% Indels: 39 DB: 3 Gaps: 1 US-10-791-017A-2 (1-656) x AK049743 (1-2269)	polyA_signal 22512256 /note="putative" polyA_site 2269 ORIGIN Alignment Scores:	/strain="C57BL/sJ" /db_xref="FANTON pis:C530046A18" /db_xref="FANTON pis:C530046A18" /clone="C530046A18" /clone="C530046A18" /tissue_type="spinal cord" /clone_lib="RIKEN full-length enriched mouse cDNA library" /dev_stage="12 days embryo" misc_feature 481903 /note="Ewing sarcoma homolog (MGD MGI:99960, GB NM_007968, evidence: BLASTN, 99%, match=2172)	Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL:http://genome.gsc.riken.jp/. URL:http://fantom.gsc.riken.jp/. FEATURES Location/Qualifiers source 1. 2269 /mol_type="mRNA"	Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GS RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yok Kanagawa 230-0045, Japan (B-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216) CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Genomic Sciences Center and Genome Science Laboratory in RIKE	Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Mateuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaki-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y. TITLE Direct Submission JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of	AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs JOURNAL Nature 420, 563-573 (2002) REFERENCE 6 (bases 1 to 2269) AUTHORS Adachi, J., Alzawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
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361 SerAlaileTyrValdInGlyLeuAsnAspSerValThrLeuAspAspLeuAlaAspPhe 380	ArgGlyGlyMetGlySerAlaGlyGluArgGlyGlyPheAsnLysProGlyGlyProMet 3	281 GluSerGlyGlyPheSerGlyProGlyGluAsnArgSerMetSerGlyProAspAsnArg 300 281 GluSerGlyGlyPheSerGlyProGlyGluAsnArgSerMetSerGlyProAspAsnArg 300	708 GGACAACAGAGTAGCTATGGTCAACAAGCAGCTATGGGCAGCAGCCTCCTACTAGTTAC 767 241 ProProGlnThrGlySerTyrSerGlnAlaProSerGlnTyrSerGlnGlnSerSerSer 260	ATGCAGCCAGTCACCGCACCTCCATCTTATCCTCCTACCAGCTACTCCTCCTTCACAGCCG ThrSerTyrAspGlnSerSerTyrSerGlnGlnAsnThrTyrGlyGlnProSerSerTyr	141 AspGlyAsnLysProThrGluThrSerGlnProGlnSerSerThrGlyGlyTyrAsnGln 160	288 ACTGCCCCGCAGGCGTACAGCCAGCCAGCCAGCCAACAGCCACCCGCACCGCACCGCACCAGCCTATGGCAGCCACGCGCACTGGGACTTATGACAGC 347 101 ThrThrAlaThrValThrThrGlnAlaSerTyrAlaAlaGlnSerAlaTyrGlyThr 120	41 TyrGlyThrTyrGlyGlnProThrAspValSerTyrThrGlnAlaGlnThrThrAlaThr 60

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Xenopus laevis, IMAGE:5543106, m
Development, 6100 Exect
20892-7510, USA
NIH-MGC Project
Contact: XGC help desk
                                              Submitted (10-JAN-2003) National Institutes of Health, Xenopus Gene Collection (XGC), National Institute of Child Health and Human Development, 6100 Executive Boulevard, Room 4801, Rockville, MD
                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Xenopus.
1 (bases 1 to 2692)
                                                                                                                                                                                         Xenopus laevis (African clawed frog)
Xenopus laevis
                                                                                               Direct Submission
                                                                                                              Klein, S. and Strausberg, R.
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Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Igor Dawid
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Lissa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.
Clone distribution: MGC clone distribution information can be found
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LIMI at: http://image.llnl.gov Series: IRAK Plate: 96 Row: j Column: 22 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein This clone has the following problem: retained intron.

Location/Qualifiers
1. 2692

	rv Match:	ca.	Percent Similarity:	Score:	Pred. No.:	Alignment Scores:
W	70.69%	71,49%	79.45%	2568.00	3.1e-147	
	Indels:	Mismatches:	Conservative:	Matches:	Length:	
19	56	96	ភភ	494	2692	

10-791-017A-2 (1-656) x BC043904 (1-2692)

Ş	1 MetAlaSerThrAspTyrSerThrTyrSerGlnAlaAlaAlaGlnGlnGlyTyrSerAla 20	20
, ;		
δλ	21 TyrThrAlaGlnProThrGlnGlyTyrAlaGlnThrThrGlnAlaTyrGlyGlnGln 39	39
D _D	71 TATACTGCACAGCCAGCTCAAGGCTACACTCAGACTGCACAGGCAACTTATGGACAGCAG	130
γ	40 SerTyrGlyThrTyrGlyGlnProThrAspValSerTyrThrGlnAlaGlnThrThrAla	59
Вb	131 AGTTATGCCCTATGCCCAGCCCAGTGATGCCAGTTACACACAGGCACAGACAG	190 -
γQ	60 ThrTyrGlyGlnThrAlaTyrAlaThrSerTyrGlyGlnProProThrGlyTyrThr 78	78
B	191 AGCTATGGGCAACAGTCTGCCTATGCCCACTTCATATGGACAGCCACCGACAGGTTACACT	250
Qγ	79 ThrProThrAlaProGlnAlaTyrSerGlnProValGlnGlyTyrGlyThrGlyAlaTyr 98	98
Db	251 GCTCCAGCTGCTCCCCAAGCCTATAGCCAGCCCATACAAGGCTATGGTTCTACAGGCTAT	310
γ	99 AspThrThrAlaThrValThrThrThrGlnAlaSerTyrAlaAlaGlnSerAlaTyr 118	118
DЬ	311 GACAGTACCACTGCAGCTACCACCACAACCCAGGCTACATATGCTGCACCCCTCTGCCTAT	370
γQ	119 GlyThrGlnProAlaTyrProAlaTyrGlyGlnGlnProAlaAlaThrAlaProThrArg 138	138
Ф	371 GGTTCCCAACCTGCATATCCTTCTTATGGTCAGCAGCCTGCTACTACTGCGTCTGCAAGA	430

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                                                                                                   GluTrpPheAspGlyLysAspPheGlnGlySerLysLeuLysValSerLeuAlaArgLys
                                                                                                                                                                                     LysProLysGlyAspAlaThrValSerTyrGluAspProProThrAlaLysAlaAlaVal
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                                 AAGCCTTTGCTAGGTAGCATGCGAGGGGGGTTGCTTTTACGTGACAGCAGAGGGCAGCCA
                                                            LysProProMetAsnSerMetArgGlyGlyLeuProProArgGluGlyArgGlyMetPro
                                                                                                                                                                     AAGCCCAAAGGAGATGGCACTGTGTCTTTTGAAGACCCACCTTCAGCTAAGACTGCTGTA
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                                                                                                                                                                                                                                                             LysMetAsnLysArgThrGlyGlnProMetIleHisIleTyrLeuAspLysGluThrGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TyrProMetGlnProValThrAlaProProSerTyrProProThrSerTyrSerSerThr
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Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishi, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
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S Adachi, J., Alzawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., S., Adachi, J., Alzawa, K., Brainci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sundan, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshino, M., Muramatsu, M., and Hayashizaki, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
Please_visit our web site (http://genome.gsc.riken.jp/) for further
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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/codon_start=3.
/proteIn_id="RAB29301.1"
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/translation="LGSAGERGGPNKPGGPMDEGPDLDLGLPIDPDEDSDNSAIYVQG
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                                                                                                putative'
                                                                                                                              /note="unnamed protein product; Ewing sarcoma homolog
                                                                                                                                                                           /dev_stage="17
<1. .1004
                                                                                                                                                                                         /tissue_type="head"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="17 days embryo"
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                                                                                                                                                                                                                                                                                                       mol_type="mRNA"
/strain="C57BL/6J"
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Search Job tin	B 8	문 왕	<u> </u>	Db
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen

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ALIGNMENTS

RESULT 1 ADASS145 ID ADASS145 XX ADAS XX ADAS XX ADAS XX ADAS XX ADAS XX CYTO XX CYTO XX Gene XX Gene XX Homo XX Homo XX 11-9 XX 21-9 Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic; Gene Therapy; human; secretory protein; membrane proteins; cancer; inflammatory disease; osteoporosis; neurological disease. 21-MAR-2002; 2002EP-00006586 EP1293569-A2 Homo sapiens Human 20-NOV-2003 19-MAR-2003. ADA55145; ADA55145 standard; protein; protein, (first SEQ ID 2713 entry) 600 8

14-SEP-2001; 2001JP-00328381. 24-JAN-2002; 2002US-0350435P. (HELI-) (REAS-) HELIX RES INST. RES ASSOC BIOTECHNOLOGY.

Isogai T, Sugiyama T, Yamamoto J, Isono Y, Seki N, Yoshikawa T, Otsuki T, Wakamatsu A, Sato H, Hio Y, Otsuka K, Nagai K, Irie Otsuka M, Nagahari K, Masuho Y; , 7 Ishii S; Tamechika H;

WPI; 2003-395539/38. N-PSDB; ADA53506.

New polynucleotides encoding full-length polypeptides, e.g. secretory and/or membrane proteins, useful for developing medicines for diseases which the gene is involved, or as target molecules for gene therapy. ij

Claim 14; SEQ ID NO 2713; 205pp; English.

The present invention relates to novel human secretory or membrane proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-ADA54071). The coding sequences are useful in the gene therapy of diseases caused by abnormalities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease.

Sequence 600 AA;

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RESULT 2
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Matches 338; Conserv
This invention relates to a novel modulators that alter the interaction between the Ewing sarcoma protein (EWS) and its nuclear receptor, as well as the screening method thereof. Specifically, it refers to determining and identifying a hormonal effect brought about by test compounds that modulate either the binding of EWS to the nuclear receptor or the ligand-
                                                                                                                                                                                                                                                                                                                                                                                                                                                              human; Ewing hypogonadism;
                                                                                                                                 Determining the hormonal effects of substances, used to identify pharmaceuticals, e.g. for treatment of androgen receptor dysfunction, from modulating interaction between nuclear receptors and Ewing sarcoma
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25-APR-2003; 2003US-0465692P.
                                                                                          Disclosure;
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                                                                                                                                                                                                                                                                       ) SCHERING
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ilarity 100.0%;
Conservative 0,
                                                                                          SEQ ID
                                                                                                                                                                                                                                         Wolf S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sarcoma; EWS; prostatic cancer; alopecia;
; androgen-resistance syndrome; testicular
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                                                                                      NO 2; 30pp; German.
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Pred. No. 5.4e-148;
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Matches 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       induced activity of this receptor. The present invention describes the nuclear receptors as including oestrogen, progesterone, thyroid hormone, Vitamin D, and retinoic acid receptors most preferably they are androgen receptors. Accordingly, these modulators may be used in the development of pharmaceutical compositions that can diagnose and be used to treat diseases associated with receptor dysfunction such as prostatic cancer, alopecia, acne, hypogonadism and androgen-resistance syndrome e.g. testicular feminisation. This method provides reliable, sensitive, simple, inexpensive and rapid assessment of the hormonal effects of these test compounds. This polypeptide sequence is the human Ewing sarcoma protein of the invention.
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                                                               ABM82330;
                                                                                              ABM82330 standard;
                              18-NOV-2004
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                                                                                              protein;
                              entry)
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Pred. No. 6e-148;
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RESULT 3
ABM82330
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IID ABM82330
IID ABM82330
AC ABM8
XX ABM8
XX Tunn
CX Tunn
KW Tunn
KW Chrc
KW Coll
KW Chrc
KW Gen

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chromosome identification; chromosome mapping;
                                                                                                                                                                             02-OCT-2002; 2002US-0414971P
                                                                                                                                                                                                                                                                                   29-SEP-2003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    therapy;
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probe; mapping;

(GETH) GENENTECH INC

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RESULT 4
ABG06460
ID ABG0
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AC ABG0
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DT 13-I
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DE NOVE
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Matches 338
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Novel human diagnostic protein #6451
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                                         13-FEB-2002
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                                                                                                                  ABG06460
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les 338; Conserv
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                                                                                                                etandard;
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Pred. No. 6e-148;
Mismatches 0
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Consequences. (I) is useful as hybridisation probes, polymerase chain
converted to the combinant production of (II). The polynucleotides are also used
converted to the combinant production of (II). The polynucleotides are also used
converted to the combinant production of (II). The polynucleotides are also used
converted to the combinant production of (II) is polynucleotides are also used
converted to the combinant production of the converted converted
converted to the co
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Matches 338;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotide and encoded polypeptides, useful diagnostics, forensics, gene mapping, identification of mutate responsible for genetic disorders or other traits and to assebiodiversity.
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23-AUG-2000;
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26-MAY-1994
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This invention relates to novel, isolated full length human cDNA CC molecules and the encoded proteins thereof. Specifically, it refers to CC cDNA clones obtained by an oligo-capting method, where none of these CC clones are identical to any known human mRNAs. The present invention CC describes an immunoassay to identify agonists and antagonists, as well as CC antibodies, antisense molecules and siRNAs that can all be used to bind CC entibodies, antisense molecules and siRNAs that can all be used to bind CC to and modulate expression of the CDNA molecules. As such, these CC molecules are useful for diagnostic markers or therapeutic targets for CC the various diseases or morbid states. In particular, they are useful in CC gene therapy for treating osteoporosis, neurological disease, Alzheimer's CC disease, Parkinson's disease, dementia, short memory and various cancers, as well as for maintaining equilibrium of sense or motor function, and CC for treating emotional reaction, fear response and panic. Accordingly, CC they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian, CC cytostatic and tranquiliser activities. This polypeptide is a protein CC encoded by a full length human cDNA sequence of the invention. NOTE: This
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Wakamatsu
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N-PSDB; ADR07446.
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09-MAY-2003; 2003JP-00131452.
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                        WPI; 1998-087086/08
                                                                                                                                                             03-JUL-1996;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EWS is a member of a novel family of putative transcription factors that have RNA recognition motifs and which are frequently associated with many types of sarcomas. It shows homology to a novel human transcriptional activity factor, Tat-stimulatory factor (Tat-SF1, see AAW33811), that is involved in the regulation of transcriptional elongation of HIV-1 by Tat, is essential for Tat trans-activation and is a substrate of an associated cellular kinase. Tat-SF can be used to screen for binding agents useful in the treatment of HIV infection
                             ABB57126 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 656 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid encoding Tat stimulating factor protein and related transformed cells - proteins and binding agents, used to treat himmunodeficiency virus infection.
ABB57126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 6; Page 47-51; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                   379
                                                                                                                 619
                                                                                                                                               301
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                                                                                                                                                                                                                                                                                                                                    121 KLKVSLARKKPPMNSMRGGLPPREGRGMPPPLRGGPGGPGGPGGPMGRMGGRGGDRGGFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                  319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GGRGGMGSAGERGGFNKPGGPMDEGPDLDLGPPVDPDEDSDNSAIYVQGLNDSVTLDDLA
                                                                                                                 GGPPGPLMEQMGGRRGGRGGPGKMDKGEHRQERRDRPY
                                                                                                                                        GGPPGPLMEQMGGRRGGRGGPGKMDKGEHRQERRDRPY
                                                                                                                                                                                                      PGGDRGRGGPGGMRGGRGGLMDRGGPGGMFRGGRGGDRGGFRGGRGMDRGGFGGGRRGGP
                                                                                                                                                                                                                                                 PRGPRGSRGNPSGGGNVQHRAGDWQCPNPGCGNQNFAQRTECNQCKAPKPEGFLPPPFPP
                                                                                                                                                                                                                                                                         PRGPRGSRGNPSGGGNVQHRAGDWQCPNPGCGNQNFAWRTECNQCKAPKPEGFLPPPFPP
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                                                                                                                                                                                                                                                                                                                 KLKVSLARKKPPMNSMRGGLPPREGRGMPPPLRGGPGGPGGPGGPMGRMGGRGGDRGGFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                             protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98.9%;
                               655
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Pred. No. 3.7e-146;
0; Mismatches 2;
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                                                                                                                656
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RESULT 8
ABB57126
ID ABB5
XX ABB5
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XX ABB5
XX MOUE
XX MOUE
XX MOUE
XX WO2(
XX WO2(
XX WO2(
XX IB-A
                                                                                                                                                                    Mouse; ischaemia; comp
vasospastic ischaemia;
           Ishikawa K,
                                                                                                     22-NOV-2001.
                                                                                                                           WO200188188-A2
                                                                                                                                                Mus musculus
                                                                                                                                                                                                     Mouse ischaemic condition related protein sequence SEQ ID NO:289.
                                                                                                                                                                                                                              07-MAR-2002
                                                       18-MAY-2000; 2000JP-00145977
                                                                             18-MAY-2001; 2001WO-JP004192
                                    VIN
           Aваi S,
                                  NIHON SCHOOL JURIDICAL PERSON
                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                 compressive ischaemia; occlusive ischaemia;
           Takahashi Y,
                                                                                                                                                                       ischaemic
                                                                                                                                                                       condition;
           Nagata T,
                                                                                                                                                                       ischaemic
              Ishii
             ĸ
                                                                                                                                                                       disease
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N-PSDB;

2002-034733/04. DB; ABI99383.

English

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RESULT 9
ADP56334
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Best Local S
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                                                                                                                                                                                     Claim 2;
               819
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                                                           438
                                                                  121
                                                                          378
                                                                                         319
                                                                                  61
                                                                                                _
                                                                                                           Similarity
                                                                                                                                                                                    Page 799-802; 2690pp;
                      GGPPGPLMEQMGGRRGGRGGPGKMDKGEHRQERRDRPY 338
                                                                                                                      655 AA;
                                                                                                       Conservative
                                                                                                                                                                             invention
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98.3%;

4.

Score 1888.5; DB 5 Pred. No. 3.2e-145; 4; Mismatches 1;

DB 5;

Human 18-NOV-2004

PRO protein sequence

SEQ ID

NO:2310.

(first entry)

immune related disease;

ADP56334 standard;

protein; 583

655

haemostatic; hepatotropic; imm nephrotropic; neuroprotective;

immunostimulant; lve; osteopathic;

200 385 140 325

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conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive schaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (ABI99202 to ABI99912, encoding the protein sequences in ABB57020 to ABB57374) or by determining the expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition improving drugs or therapeutics for ischaemic diseases. ABI99913 and ABI99914 represent PCR primers for a mouse ischaemic condition related sequence, which are used in the exemplification of the present invention
                                                                  immune response stimulation; antiallergic; antianaemic; antiarthri antiasthmatic; antidiabetic; antiinflammatory; antipsoriatic; antitheumatic; antithyroid; CNS; dermatological; gastrointestinal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRGPRGSRGNPSGGGNVQHRAGDWQCPNPGCGNQNFAWRTECNQCKAPKPEGFLPPPFPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KLKVSLARKKPPMNSMRGGLPPREGRGMPPPLRGGPGGPGGPGGPMGRMGGRGGDRGGFF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRGPRGSRGNPSGGGNVQHRAGDWQCPNPGCGNQNFAWRTECNQCKAPKPEGFLPPPFFP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                describes a method for examining
                                                                                                                 inflammatory immune response;
lergic; antianaemic; antiarthritic;
                                         immunosuppressive; muscular;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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of particular
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                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local &
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Wood WI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New PRO polynucleotides and polypeptides, useful and treating an immune related disease, e.g. systerythematosus, rheumatoid arthritis, diabetes mei
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 2310; 3009pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ADP56333.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRO protein
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                                                                                           141
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r S,
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                                                                                                                                                                       HIYLDKETGKPKGDATVSYEDPPTAKAAVEWFDGKDFQGSKLKVSLARKKPPMNSMRGGL
                                                                            PPREGRGMPPPLRGGPGGPGGPGGPMGRMGGRGGDRGGFPPRGPRGSRGNPSGGGNVQHR
AGDWQCPNPGCGNQNFAWRTECNQCKAPKPEGFLPPPFPPPGGDRGRGGPGGMRGGRGGL
                                                                                                                                            HIYLDKETGKPKGDATVSYEDPPTAKAAVEWFDGKDFQGSKLKVSLARKKPPMNSMRGGL
                                                                                                                                                                                                                                       PMDEGPDLDLGPPVDPDEDSDNSAIYVQGLNDSVTLDDLADFFKQCGVVKWNKRTGQPMI
                                                                                                                                                                                                                                                                PMDEGPDLDLGPPVDPDEDSDNSAIYVQGLNDSVTLDDLADFFKQCGVVKMKKTGQPMI
                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                Ä
                                                                                                                                                                                                                                                                                                                                                        94.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        describes an isolated PRO nuc
or comprising (I); (2) a host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gurney
                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                  Score 1810; DB 8;
Pred. No. 7e-139;
0; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             eful in useful in diagnosing systemic lupus
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         The invention relates to human tumour-associated antigenic target (TAT)

polypeptides, and their related nucleic acids. The TAT polypeptides are

overexpressed in cancer tissues compared to normal tissues, and may thus

serve as effective targets for the diagnosis and treatment of cancer in

mammals. The invention also relates to nucleic acid and polypeptide

sequences at least 80% identical to the TAT nucleic acids and

caid; an antibody specific for a TAT polypeptide; a peptide or organic

molecule which binds to a TAT polypeptide; fuelon proteins comprising a

TAT polypeptide; and methods and compositions for the treatment or

diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,

antibodies, antagonists, binding molecules and compositions are useful

for diagnosis or treating a cell proliferative disporder associated with

increased TAT expression, particularly cancers such as breast cancer,

cancer, pancreatic cancer, overvina cancer, liver cancer, bladder

cancer, pancreatic cancer, overvina cancer, and gene mapping, in

nervous system, melanoma and leukaemia. TAT nucleic acids may further be

used as hybridisation probes, in chromosome and gene mapping, in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumour-associated antigenic target; TAT; human; overexpression; cumour; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoma; leukaemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping;
                                                                                                                                                                                                                                                                                                                                                                                                  New tumor-associated antigenic target polypeptides and nucluseful in preparing a medicament for treating or detecting proliferative disorder, e.g. breast, lung, colorectal, ovar
                                                                                                                                                                                                                                                                                                                                                  Claim 12; SEQ ID NO 491; 7273pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-OCT-2002; 2002US-0414971P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-SEP-2003; 2003WO-US028547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-NOV-2004
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                                                                                                                                                                                                                                                                                                                                                                                         cancer or tumor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MDRGGPGGMFRGGRGGDRGGFRGGRGMDRGGFGGGGRRGGPGGPPGPLMEQMGGRRGGRGG 320
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RESULT 11
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ID ABG95
XX ABG95
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XW Proli
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Best Local S
Matches 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chromosome aberration; oncogenic fusion protein; cancer; proliferative disease; cellular protein isoform; heat shock protein 9: HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder; T cell lymphona; B cell lymphoma; chronic myeloid leukaemia; CML; acute myeloid leukaemia; AML; chronic myeloid leukaemia; CMML; acute lymphoblastic leukaemia; AL; APL; NHL; solid tumour; papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma; rhabdomyosarcoma; synovial sarcoma; viral infection.
                                                                                                                                                                                                                                                                                                                                    01-MAR-2001; 2001US-0272751P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-SEP-2002.
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                                                                                                                                        2002-698710/75
DB; ABS73274.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KLKVSLARKKPPMNSMRGGLPPREGRGMPPPLRGGPGGPGGPGGPMGRMGGRGGDRGGFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DFFKQCGVVKMNKRTEQPMIHTYLDKETRKPKGDATVSCEDSPTAKAAVEWFDGKDFQGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DFFKQCGVVKMNKRTGQPMIHIYLDKETGKPKGDATVSYEDPPTAKAAVEWFDGKDFQGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGPPGPLMEQMGGRRGGRGGPGKMDKGEHRQERR 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PGGDRGRGGPGGMRGGRGGLMDRGGPGGMFRGGRGGDRGGFRGGRGMDRGGFGGGRRGGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----LVEE----DKVALGGPRTFDVTNGRKKRR 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PGGDHGRGGPGGMWGGRGGLMDHGGPGGMFRGGCGRDRSGFCGGWAWTEVA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRGPQGSRGNTSGGGNVQHQAGDRQCPNPGCGNQNFAWRTESNKCKAPKPEGFLPPPFPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KLKVSLARKRPPVNSMQGGMPPHEGRGMPPPLCGGPGGPGSPGGPMGHMGGRGGDRGGLP
                                                                                                                                                                                                                         Burrows
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78.1%;
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Pred. No. 6.3e-107;
4; Mismatches 41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90;
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Treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins, e.g. cell prolif diseases, involves administering an inhibitor of heat shock prot

cell proliferative shock protein 90.

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Disclosure;
 Page 228-229;
389pp; English.
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administering HSP90-inhibitor. The method is useful for treating genetically-defined disease with chromosomal aberration yielding oncogenic fusion protein, treating cancerous cells containing fusion protein in heterogeneous cell population, treating proliferative disease (e.g. rheumatoid arthritis or cancer) associated with mutant protein or cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g. p53), or selectively treating cells expressing mutant protein or cellular protein isoform in a patient heterozygous for (II). The method is useful for treating a disease e.g. haematopoletic disorder such as T or B cell lymphoma, chronic myeloid leukaemia (CML), APL, ALL, AML, NHL and CMML, or a disease characterised by a solid tumour such as papillary thyroid carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and synovial sarcoma. The method is also useful for treating viral infections. This represents a protein encoded by the DNA sequence of a The invention describes a method of treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins (I), treating cancerous cells containing (I) in a heterogeneous cell population, treating proliferative diseases associated in the containing (I) and the containing containing treating proliferative diseases associated in the containing containing the containing contain pulation, treating proliferative diseases associated with mutant or cellular protein isoforms (II) dependent on heat shock protein 0, or selectively treating cells expressing (II) involving tering HSP90-inhibitor. The method is useful for treating aberration

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Best Local S
Matches 182
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                                                                                                                              PRGPRGSRGNESGGGNVQHRAGDWQCFNPGCGNQNFAWRTECNQCKAPKPEGFLPPPPPPPP
                                                                                                                                                                                                                                                                                         GRGGMGGS-DRGGFNKFGGPRDQGSRHD----SEQDNSDNNTIFVQGLGENVTIESVA
                                                                                                                                                                        PIKVSFATRRADFN--RGGGNGRGGRG----RGGPMGRGGYGGG----GSGGGGRGGFP
                                                                                                                                                                                                   KLKVSLARKKPPMNSMRGGLPPREGRGMPPPLRGGPGGPGGPGGPMGRMGGRGGDRGGFP
                                                                                                                                                                                                                                   DYFKQIGIIKTNKKTGQPMINLYTDRETGKLKGEATVSFDDPPSAKAAIDWFDGKEFSGN
                                                                                                                                                                                                                                               DFFKQCGVVMMKRTGQPMIHIYLDKETGKPKGDATVSYEDPFTAKAAVEWFDGKDFQGS
                                                                                                                                                                                                                                                                                                                       GGRGGMGSAGERGGFNKPGGPMDEGPDLDLGPPVDPDEDSDNSAIYVQGLNDSVTLDDLA
                           RRGGPGGPPGPLMEQMGGRRGGRGGPGKMD-KGEHRQERRDRPY 338
                                                                                     PGGDRGRGGPGGMR-GGRGGLMDRGGPGGMFRG---GRGGDRGGFRGGR-GMDRGGFGGG 295
                                                                                                                 SGG-----
                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                        - GGPGGSHMGGNYGDDRRGGRGGYDRGGYRGRGGDRGGFRGGRGGGDRGGF---
                                                                                                                                                                                                                                                                                                                                                                  45.7%;
                                                                                                                 -GGGGGQQRAGDWKCPNPTCENMNFSWRNECNQCKAPKPDG------
                                                                                                                                                                                                                                                                                                                                                    36;
                                                                                                                                                                                                                                                                                                                                                 Score 878; DB 5; 1
Pred. No. 5.6e-63;
6; Mismatches 54;
-GPGKMDSRGEHRQDRRERPY
                                                                                                                                                                                                                                                                                                                                                                                Length 525;
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RESULT 12
ADR14649
 ADR14649 standard;
protein;
  525
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21-OCT-2004 (first entry)

Human NF-kappaB pathway-associated protein SeqID650.

NF-kappaB pathway; antiinflammatory; cytostatic; hepatotropic; virucide; antiarthritic; antirheumatic; gastrointestinal-Gen; antiasthmatic; antiarteriosclerotic; immunomodulator; cerebroprotective; vasotropic; immunosuppressive; vulnerary; gene therapy; immune disorder; inflammatory disorder; NF-kappaB regulation; Cancer; aberrant apoptosis; hepatic disorder; Hodgkin's lymphoma; haematopoletic tumour; hyportopic; hyper-IgM syndrome; hypohidrotic ectodermal dysplasia; dysplasia;

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61

DFFKQCGVVKMNKRTGQPMIHIYLDKETGKPKGDATVSYEDPPTAKAAVEWFDGKDFQGS GGRGGMGGS-DRGGFNKFGGPRDQGSRHD----SEQDNSDNNTIFVQGLGENVTIESVA GGRGGMGSAGERGGFNKPGGPMDEGPDLDLGPPVDPDEDSDNSAIYVQGLNDSVTLDDLA 60

248

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Query Match Best Local & Matches

Local Similarity

45.7%; Score 878; DB 8; 52.9%; Pred. No. 5.6e-63; tive 36; Mismatches 54

Length 525 Indels

72;

301

Conservative

Sequence

525

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This invention relates to the novel association of protein sequences (and CC the genes which encode them) to the NF-kappaB pathway. The invention may CC be useful for the production of compounds with an antiinflammatory, CC cytostatic, hepatotropic, virucide, antiarthritic, antiinflammatory, CC gastrointestinal-Gen, antiasthmatic, antiarteriosclerotic, cumunomodulator, cerebroprotective, vasotropic, immunosuppressive or vulnerary activity or for gene therapy. The proteins and nucleotides are useful for diagnosing, preventing, treating, or ameliorating conditions cor diseases associated with the NF-kappaB pathway. The condition is an immune disorder, an inflammatory disorder an inflammatory disorder an inflammatory disorder and immune disorder, hedgkin's lymphomas, haematopoietic tumours, hyper-IgM syndromes, hypohidrotic ectodermal dysplasia, x-linked anhidrotic cordermal responses, rheumatorid arthritis, inflammatory bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick syndrome, stroke, EAE, autoimmune disorders, disorders related to hyper immune activity, disorders related to aberrant acute phase responses, corgan transplant rejection, conditions related to organ transplant corders, cancers and HIV propagation in cells infected with other viruses. The present sequence is that of a human protein which is subject to the novel association with the NF-kappaB pathway of the condition but was obtained by the indexer from Genbank.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotides and polypeptides associated with NF-kappaB pathway, useful for diagnosing, treating, or preventing disorders or diseases associated with NF-kappaB pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aberrant acute phase response; hypercongenital condition; birth defect; necrotic lesion; wound; organ transplant rejection; aberrant signal transduction; proliferating disorder; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     viral infection; HIV-1; HTLV-1; hepatitis B; hepatitis C; EBV; influenza; viral replication; host cell survival; evasion of immune response; rheumatoid arthritis; inflammatory bowel disease; colitis; asthma; atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE; autoimmune disorder; hyper immune activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-JAN-2003; 2003US-0440068P.
12-MAY-2003; 2003US-0469757P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
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PR 03-PI
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                   The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation. The production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities,
                                                                                                                                                                                                                                                                                                                                                                                                   Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; cytokine; cell proliferation; cell differentiation; gene the vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                  Nucleic acids encoding in diagnosis and gene t
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27-APR-2000;
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19-JUL-2000;
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, Zhao QA, Wang D, I
AJ, Yang Y, Wejhrman
    etem
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DB; AAK51488.
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                                                                                                                                                                                      Page 3253-3254; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; 2000US-00496914.
; 2000US-00560875.
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; 2000US-00620325.
; 2000US-00624936.
; 2000US-00693355.
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factor activity, haematopoiesis
                                                                                                                                                                                                                                     polypeptides with cytokine-like
therapy.
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Wang
n T,
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JJ, Zhang J,
Goodrich R;
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J, Ren
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     WPI; 2002-698710/75.
N-PSDB; ABS73271.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
                                                                                                                                                                                                                                                       01-MAR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human translocation (12; 16)(q13; p11) protein
                                                                                                                                                                                                 01-MAR-2001; 2001US-0272751P
                                                                                                                                                                                                                                                                                                           12-SEP-2002
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tive 36; Mismatches 54
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PIKVSFATRRADFN--RGGGNGRGGRG---

GSGGGGRGGFP

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The invention relates to a purified protein promoting signal transducer and activator of transcription 6 activation (STAT6). The protein is cuseful for the producing an antibody, which involves administering the protein or its epitope-bearing fragments to a non-human animal as an cantigen. The nucleic acid is useful for diagnosing a disease or compounds which inhibit or promote STAT6 activation. A transformant expressing the protein is useful for screening compounds which inhibit or promote STAT6 activation. A transformant composition is useful for producing a pharmaceutical composition. Compositions, antibodies and antisense molecules are useful for treating a disease associated with STAT6 activation such as allergic disease, inflammation, autoimmune diseases, diabetes, composition disease and cancers. Compositions are useful for treating disease associated with STAT6 activation and/or prevention of fhi hyperactive diseases. Compositions are also useful in rheumatoid carthritis, osteoarthritis, systemic lupus erythematosus, sepsis, asthma, composition of storation and and and and and are represented with storation are useful for treating and and and and and and are represented with storation are useful for treating and and and and and and are represented with storation are diseases. Compositions are also useful for screening compounds for treating and preventing disease associated with excessive activation or inhibition of STAT6. The present sequence represents the amino acid sequence of a human protein which promotes STAT6 activation.
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Best Local
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06-JUN-2002; 2002US-0385912P.
26-DEC-2002; 2002JP-003J7326.
27-DEC-2002; 2002US-0436467P.
15-MAY-2003; 2003JP-00137505.
16-MAY-2003; 2003US-0470836P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New signal transducer and activator of transcription 6 activation promoting purified protein, for diagnosing and treating disease associated with activation/inhibition of transcription factor e.g diabetes and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rheumatoid arthritis; osteoarthritis; systemic lupus erythematosus; sepsis; asthma; allergic rhinitis; ischaemic heart disease; subarachnoid haemorrhage; viral hepatitis; AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; ADI26116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sugahara
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                                                                                                                                                                                                                                                                                 Sequence 526
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KLKVSLARKKPPMNSMRGGLPPREGRGMPPPLRGGPGGPGGPGGPMGRMGGRGGDRGGFP
                                            DYFKQIGIIKTIKKTGQPMINLYTDRETGKLKGEATVSFDDPPSAKAAIDWFDGKEFSGN
                                                                                 DEFKOCGVVKMNKRTGOPMIHIYLDKETGKPKGDATVSYEDPFTAKAAVEWEDGKDFOGS
                                                                                                                          GGRGGMGGS-DRGGFNKFGGPRDQGSRHD----SEQDNSDNNTIFVQGLGENVTIESVA
                                                                                                                                                               GGRGGMGSAGERGGENKPGGPMDEGPDLDLGPPVDPDEDSDNSAIYVQGLNDSVTLDDLA
                                                                                                                                                                                                                                                                                   AA;
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                                                                                                                                                                                                      Score 878; DB 8;
Pred. No. 5.6e-63;
6; Mismatches 54
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                                                                                                                                                                                                                                            Length 526;
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Search Job tim	문	ş	DЬ	ঠ	뭣	8
Search completed: February 18, 2005, 15:27:34 Job time : 166 secs	507	296 RRGGPGGPPGPLMEQMGGRRGGPGKMD-KGEHRQERRDRPY 338	455 PGGGPGGSHMGGNYGDDRRGGRGGYDRGGYRGRGGDRGGFRGGRGGGDRGGF 506	241 PGGDRGRGGPGGMR-GGRGGLMDRGGPGGMFRGGRGGDRGGFRGGR-GMDRGGFRGG 295	412 SGGGGGGGQQRAGDWKCPNPTCENMNFSWRNECNQCKAPKPDG 454	181 PRGPRGSRGNPSGGGNVQHRAGDWQCPNPGCGNQNFAWRTECNQCKAPKPEGELPPPFPP 240

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
Score
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Match
BLOSUM62
Gapop 10.0 , Gapext 0.
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1922
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| /ggn2_6/ptodata/1/laa/5A_COMB.pep:*
| /ggn2_6/ptodata/1/laa/5B_COMB.pep:*
| /ggn2_6/ptodata/1/laa/6B_COMB.pep:*
| /ggn2_6/ptodata/1/laa/6B_COMB.pep:*
| /ggn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
| /ggn2_6/ptodata/1/laa/PcTUS_COMB.pep:*
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US-08-343-443B-2
US-09-214-542A-4
US-09-238-092-1126
US-09-949-016-10914
US-09-949-016-7825
US-09-949-016-7825
US-09-538-092-1080
US-08-963-825-21
US-09-570-811-21
US-09-548-608-21
US-09-548-608-21
US-09-949-016-8369
US-08-68-96-12
US-08-963-825-72
US-09-588-963-18
US-09-588-608-18
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       Sequence 2, Appli
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Sequence 10515, Ap
Sequence 10915, Ap
Sequence 1080, Ap
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Sequence 21, Appli
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Sequence 12, Appli
Sequence 13, Appli
Sequence 14, Appli
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Sequence 21, Appli
Sequence 21, Appli
Sequence 31, Appli
Sequence 31, Appli
Sequence 47, Appli
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APPLICANT:	APPLICANT:	APPLICANT:	APPLICANT:	APPLICANT:	GENERAL INFORMATION:	t No. 596	Sequence 2, Ap	US-08-343-443B-2	1		253	253	253	257	258	258	258	258.5	258.5	258.5	258.5	258.5	258.5	259	259	. 260	261.5	262
Peter, Martin	Melot,	Desmaze,	Delattre, Olivier	Aurias,	MATION:	8734	, Application US/08343443B				13.2	13.2	13.2	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.5	13.5	13.5	13.6	13.6
Martine	Thomas), Chantal	e, 01	Alain			n US/				1442	1442	274	599	1670	1609	689	1418	1418	1418	1418	1418	1060	1057	1017	633	1806	822
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ממקטעווים לובוצורינוטות במיניטי.	
INFORMATION FOR SEQ ID NO: 2:	٠.
TELEFAX: 215-875-8394	٠.
L/J	٠.
TELECOMMUNICATION INFORMATION:	٠.
REFERENCE/DOCKET NUMBER: 989.6121P	٠.
REGISTRATION NUMBER: 19,763	٠.
NAMB: Weiser, Gerard J.	٠.
	٠.
FILING DATE: 20-MAY-1992	٠.
APPLICATION NUMBER: FR 92/06123	٠.
PRIOR APPLICATION DATA:	٠.
FILING DATE: 19-MAY-1993	٠.
APPLICATION NUMBER: PCT/FR93/00494	٠.
PRIOR APPLICATION DATA:	٠.
CLASSIFICATION: 514	٠.
FILING DATE: 18-NOV-1994	٠.
APPLICATION NUMBER: US/08/343,443B	٠.
CURRENT APPLICATION DATA:	٠.
SOFTWARE: AEDIT 1.0 DOS text editor	٠.
OPERATING SYSTEM: PC-DOS/MS-DOS	٠.
COMPUTER: IBM PC compatible	٠.
MEDIUM TYPE: Floppy disk	٠.
COMPUTER READABLE FORM:	٠.
ZIP: 19102	٠.
COUNTRY: USA	٠.
	٠.
_	٠.
::	٠.
ADDRESSEE: Weiser & Associates	٠.
CORRESPONDENCE ADDRESS:	٠.
NUMBER OF SEQUENCES: 129	٠,
TITLE OF INVENTION: TRANSLOCATIONS	٠.
OF INVENTION:	٠.
OF INVENTION:	٠.
INVENTION:	٠.
	٠.
: Zucman,	٠.
	٠.
APPLICANT: Ploougastel, Beatrice	٠.
••	٠.
: Melot, T	٠.
••	••
••	٠.
APPLICANT: Aurias, Alain	٠.

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; LENGTH: 656 amino aci
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-343-443B-2
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US-09-214-564A-4
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ORGANISM: Homo sapiens
US-09-214-564A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 338; Conserv
                                                                                                                                                                                                                                                                                  SOFTWARE:
SEQ ID NO 4
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                                                                                                                                           Matches
                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                APPLICANT: Sharp, Phillip A.

APPLICANT: Zhou, Qiang
TITLE OF INVENTION: TAT-SF: Cofactor For Stimulation Of Transcriptional
TITLE OF INVENTION: Elongation By HIV-1 TAT
FILE REFERENCE: M0656/7042
CURRENT PELICATION NUMBER: US/09/214,564A
CURRENT FILING DATE: 1999-08-18
PRIOR APPLICATION NUMBER: US 60/021,218
PRIOR FILING DATE: 1996-07-03
PRIOR FILING DATE: 1996-07-03
PRIOR PILING DATE: 1996-12-13
PRIOR APPLICATION NUMBER: US 60/033,152
PRIOR PILING DATE: 1996-12-13
PRIOR APPLICATION NUMBER: PCT/US97/11713
PRIOR FILING DATE: 1996-12-03
PRIOR FILING DATE: 1997-07-03
NUMBER: OF SEQ ID NOS: 5
                                                                                                                                                                                                                                                                  LENGTH: 656
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379
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                                   61
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FastSEQ for Windows Version 3.0
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                    DFFKQCGVVXMKKTGQPMIHIYLDKETGKPKGDATVSYEDPTAKAAVEWFDGKDFQGS 120
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                                                                                       GGRGGMGSAGERGGFNKPGGPMDEGPDLDLGPPVDPDEDSDNSAIYVQGLNDSVTLDDLA
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ilarity 100.0%;
Conservative 0
                                                                                                                                         100.0%; Score 1922; DB 3; llarity 100.0%; Pred. No. 1.7e-150; Conservative 0; Mismatches 0;
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Pred. No. 1.7e-150;
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APPLICANT: Glot, Loic
APPLICANT: MAINFIELD, Traci A.
APPLICANT: MAINFIELD, Protein-Protein Complexes and
TITLE OF INVENTION: Protein-Protein Complexes and
TITLE OF INVENTION: Protein-Protein Complexes and
TITLE OF INVENTION NUMBER: US/09/538,092
CURRENT APPLICATION NUMBER: 60/127,352
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuraPatSegFormatter Version 0.9
SEQ ID NO 1250
LENGTH: 656
TYPE: PRT
TOPNATION: Homo samiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number Q01844
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRGPRGSRGNPSGGGNVQHRAGDWQCPNPGCGNQNFAWRTECNQCKAPKPEGFLPPPPPP 240
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US-09-949-016-10914
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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Best Local S
Matches 318
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 6812339 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10915, Application US/09949016
APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

FILE REFERENCE: CL001307

FILE REFERENCE: CL001307

FILE REFERENCE: CU00-104-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-09

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-10-03

PRIOR FI
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LENGTH: 591
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SOFTWARE: FastSEQ for Windows Version
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100.0%; Pred. No. 2.6e-141;
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                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Human US-09-949-016-10915
                                                                                                                                                                                        Best Loc
Matches
                                                                                                                                                                                                                                                                                SOPTWARE: FastSEQ for Windows Version
SEQ ID NO 7825
LENGTH: 306
TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7825, Application US/09949016
Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 318; Conservative
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LENGTH: 591
                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                         Local Similarity
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141 PPREGRGMPPPLRGGPGGPGGPGGPMGRMGGRGGDRGGFPPRGPRGSRGNPSGGGNVQHR
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                                                          HIYLDKETGKPKGDATVSYEDPPTAKAAVEWFDGKDFQGSKLKVSLARKKPPMNSMRGGL
                                     HTYLDKETRKPKGDATVSCEDSPTAKAAVEWFDGKDFQGSKLKVSLARKRPPVNSMQGGM
                                                                                                             MDRGGPGGMFRGGRGGDRGGFRGGRGMDRGGFGGGRRGGPGGPPGPLMEQMGGRRGGRGG
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100.0%; Pred. No. 2.6e-141;
                                                                                                                                                                                      69.6%; Score 1337; DB 4; 78.3%; Pred. No. 1.3e-102; 2ive 13; Mismatches 37;
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 1080
                                                                                                                                                                                                                                                                                                                                                                                                             Matches 182;
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CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuraPatSeqFormatter Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Giot, Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number P35637
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ORGANISM: Homo sapiens
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                                 RRGGPGGPPGPLMEQMGGRRGGRGGPGKMD-KGEHRQERRDRPY 338
                                                                                                                                                                   PRGPRGSRGNPSGGGNVQHRAGDWQCPNPGCGNQNFAWRTECNQCKAPKPEGFLPPPFPP 240
                                                                                                                                                                                                                                      KLKVSLARKKPPMNSMRGGLPPREGRGMPPPLRGGPGGPGGPGGPMGRMGGRGGDRGGFP 180
                                                                                                                                                                                                                                                                         GGRGGMGSAGERGGFNKPGGFMDEGFDLDLGPFVDFDEDSDNSAIYVQGLNDSVTLDDLA
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                                                                                                    PGGDRGRGGPGGMR-GGRGGLMDRGGPGGMFRG---GRGGDRGGFRGGR-GMDRGGFGGG 295
                                                                                                                                                                                                        PIKVSFATRRADFN--RGGGNGRGGRG----RGGPMGRGGYGGG----GSGGGGRGGFP
                                                                                                                                                                                                                                                                                                                                          GGRGGMGGS-DRGGFNKFGGPRDQGSRHD----SEQDNSDNNTIFVQGLGENVTIESVA
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52.9%; Pred. No. 1.7e-64;
tive 36; Mismatches 54
                                                                                                                                     GGGGGQQRAGDWKCPNPTCENMNFSWRNECNQCKAPKPDG---
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RESULT 8

RESULT 9 US-08-963-825-21

Sequence 21, Application US/08963825 Patent No. 6110689 GENERAL INFORMATION: APPLICANT: Qvist, Per

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                                                                                                                                   Matches
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Best Local (
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INFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER: PCT/FF
FILING DATE: 19-MAY-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 92/
FILING DATE: 20-MAY-1992
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                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 86 amino acids
                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Welser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: AEDIT 1.0 DOS text editor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/343,443B
FILLING DATE: 18-NOV-1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: ZUGMAN, JESSICA

TITLE OF INVENTION: NUCLEIC ACID CORRESPONDING TO A GENE OF
TITLE OF INVENTION: CHROMOSOME 22 INVOLVED IN RECURRENT CHROMOSOMAL
TITLE OF INVENTION: TRANSLATIONS ASSOCIATED WITH THE DEVELOPMENT OF CANCEROUS
TITLE OF INVENTION: TUMORS, AND NUCLEIC ACIDS OF FUSION RESULTING FROM SAID
TITLE OF INVENTION: TRANSLOCATIONS
TITLE OF INVENTION: TRANSLOCATIONS

NUMBER OF SEQUENCES: 129
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CITY: Phi
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TOPOLOGY:
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ZIP: 19102
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                   105 AKAAVEWFDGKDFQGSKLKVSLARKK 130
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61
                                                                              45 IYVQGLNDSVTLDDLADFFKQCGVVKMKRTGQPMIHIYLDKETGKPKGDATVSYEDPPT 104
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                                                                  IYVQGLNDSVTLDDLADFFKQCGVVKMKRTGQFMIHIYLDKETGKFKGDATVSYEDFFT
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230 South Fifteenth Street
                                                                                                                                    Conservative
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Thomas, Gilles
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Desmaze, Chantal
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100.0%; Pr
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                                                                                                                                 k; Score 453; DB
k; Pred. No. 2.5
0; Mismatches
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86
                                                                                                                                   2.5e-30;
hes 0;
                                                                                                                                                                    DB 2;
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US-08-963-825-21
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Best Local Similarity
Matches 115; Conserv
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CLASSIFICATION: 436
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US/08/
APPLICATION NUMBER: 21-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 236687
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Home
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-77000
TELEPHAX: 212-753-6237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 21-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: GOGOTIS, Adda C
REGISTRATION NUMBER: 29,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                   KLKVSLARKKPPMNSMRG--GLPPREGRGMPPPLRGGPGGPGPG-----GPMGRMG--G 171
                                                                                                                                                                                                                                                                                                                                                                 DFFKQCGVVKMNKRTGQPMIHIYLDKETGKPKGDATVSYEDPPTAKAAVEWFDGKDFQGS 120
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APGAPGGKGDAGAPGERGPPGLAGAPGLRGGAG-PPGPEGGKGAAGPPGPPGAAGTPGLQ
                                     --GGPGGMFRGGRGGDRG-----GFRGGRGMDRGGFGGGRRGGPGGPPG----PLME
                                                                                                                                                                                                   RGGDRGGFPPRGPRGSRG-----NPSGGGNVQHRAGDWQCPNPGCGNQNFAWRTECNQCK 226
                                                                                                                   APKPEGELPPPFPP----PGGDRGRGGPGGMRG-----GRGGLMDR------
                                                                                                                                                                                                                                             ----RGAPGPAGPRGAAGEPGRDGVPGGPGMRGMPGSPGGPGSDGKPGPPGSQGESG
                                                                             PPGKNGEYGPQGPPGPTGPGGDKGDTGPRGPQGLQGLPGTGGPPGENEKPGEPGPKGEAG
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805 Third Avenue
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in Body Fluids, A Test Kit and Means for Carrying Out
Method and Use of the Method to Diagnose the Presence
Disorders Associated with the Metabolism of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15.8%; Score 303; DB 3 30.3%; Pred. No. 1e-16;
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GENERAL INFORMATION:
                                                                                                                                                                                                                                         Matches 115;
                                                                                                                                                                                                                                                                            Query Match
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CTONE: COLLAGEN ALBUA
                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Gogoris, Adda C
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE
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 172 RGGDRGGFPPRGPRGSRG---
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                                                                 KLKVSLARKKPPMNSMRG--GLPPREGRGMPPPLRGGPGGPGGPG-----GPMGRMG--G
                                                                                                                                                                                                       GGRGGMGSAGERGGFNKPGGPMDEGPDLDLGPPVDPDEDSDNSAIYVQGLNDSVTLDDLA 60
                                                                                                                                                                       GAKGEPGPRGERGEAGIPGVPGAKGEDGKDGSPGDPGANGLPGAAGERGALGS----
                                                                                                                                                                                                                                                                                                                            COLLAGEN ALPHA 1 (III)
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                                 RGAPGPAGPRGAAGEPGRDGVPGGPGMRGMPGSPGGPGSDGKPGPPGSQGESG
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                                                                                                                                                                                                                                                         15.8%;
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in Body Fluids, A Test Kit and Means for
Method and Use of the Method to Diagnose
Disorders Associated with the Metabolism
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                                                                                                                                                                                                                                         15; Mismatches
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                                                                                                                                                                                                                                                         Score 303; DB 3
Pred. No. 1e-16;
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--- NPSGGGNVQHRAGDWQCPNPGCGNQNFAWRTECNQCK 226
                                                                                                 -RGPAGPNGIPGEKGPAGE-----
                                                                                                                                                                                                                                                                         DB 3;
                                                                                                                                                                                                                                          126;
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the Presence
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                                                                         Query Match
Best Local
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GENERAL INFORMATION:
                                                          Matches
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                                                                                                                                                                                                                                                                                                            TELEX: 236687
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: TEM PC DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                   MOLECULE TYPE: 1
ORIGINAL SOURCE:
ORGANISM: Hom
                                                                                                                                                                                                                                                                                                                                                                   NAME: Gogoris, Adda C
REGIENCE 29,714
REFERENCE DOCKET NUMBER: 43
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
                                                                                                                                             IMMEDIATE SOURCE:
CLONE: COLLAGEN ALPHA 1 (III)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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                                                      hes 115;
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                                                                         Similarity
                                                                                                                                                                                                                                                           amino acid
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in Body Fluids, A Test Kit and Means for Carrying Out
Method and Use of the Method to Diagnose the Presence
Disorders Associated with the Metabolism of
                                                      15.8%; Score 303; DB 3 30.3%; Pred. No. 1e-16; tive 15; Mismatches 1
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                                                                                          DB 3; Length 1078;
                                                        126;
                                                        Indels 124;
                                                          Gaps
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US-09-548-608-21
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:

NAME: GOGOTIS, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 430
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 01
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
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                                                                          TOPOLOGY: linear
                                                                                                                                                    LENGTH:
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in Body Fluids, A Test Kit and Means for
Method and Use of the Method to Diagnose
Disorders Associated with the Metabolism
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CLONE: COLLAGEN ALPHA 1 (III)
US-09-548-608-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application Patent No. 6010863 GENERAL INFORMATION:
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                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 1057 amino acids
                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                            ORIGINAL SOURCE:
                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
NAME/KEY: Modified-site
LOCATION: 1055
OTHER INFORMATION: /label= Modified
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                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
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                                                                                          ORGANISM:
                                                                      TISSUE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RPGPPG---PSGPRGQPGVMGFPGPKGNDGAPGKNGERGGPG-GPGPQG------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----RGAPGPAGPRGAAGEPGRDGVPGGPGMRGMPGSPGGPGSDGKPGPPGSQGESG
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                                                                      Homo sapiens
PE: Collagen type
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US-09-949-016-8369
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                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 8369
LENGTH: 955
                                                                                                                                                    Query Match
Best Local Similarity
Matches 123; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: VENTER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8369, Application US/09949016 Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity Matches 116; Conserv
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                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: CL001307
CURRENT APPLICATION NUMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                        TYPE: PRT
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    614
                                                                          555 GGSGGSPDGAGGSKLPPVLANLMGSMGAGKGPQGPGGGGINVQEILTSIMGSPNSHPSE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                310 OMGGRRGGRGGPG-KMDKGE 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          264 --GGPGGMFRGGRGGDRG-----GFRGGRGMDRGGFGGGRRGGPGGPPG----PLME 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  459
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                                      40 SDNSAIYVQGLNDSVTLDDLADFFKQCGVVKWNKRTGQPMIHIYLDKETGKPKGDATVSY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DFFKQCGVVKMNKRTGQPMIHIYLDKETGKPKGDATVSYEDPPTAKAAVEWFDGKDFQGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAKGEPGPRGEAGIPGVPGAKGEDGKDGSPGEP-----GAN-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPGKNGETGPQGPPGPTGPGGDKGDTGPPGPQGLQGLPGTGGPPGENGKPGEPGPKGDAG
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                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                 for Windows Version
                                                                                                                                                  13.9%; Score 266.5; DB 4; 30.8%; Pred. No. 9.2e-14; cive 19; Mismatches 143;
    -ELLKQPDYSDKIKQM-LVPHGLLGPGPIANGFPPGGPGGPKG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.7%; Score 301; DB 3; 30.5%; Pred. No. 1.5e-16; tive 15; Mismatches 125
                                                                                                                ---MGSAGERGGFNKPGG---PMDEGPDLDLGPP-VDPDED
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                                                                                                                                                      Indels
                                                                                                                                                                                          Length 955;
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1340 GEPGTDGAAGKEGPPGKOGPYGPPGPKGDPGAAGOKGOAGEKGRAGMP-GGPGKSGSMGP	ይ \$
OBUSTAN TOTAL TOTA	?
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222 CNQCKAPKPEGFLPPPFPPPGGDRGRGGPGG	Ş
b 1243 FKGKTGHPGLPGPKGDCGKPGPPGSTGRPGAEGEPGAMGPQG 1284	B
171 GRGGD	Ś
1184	B
y 115 KDPQG\$KLKV\$LARKKPPMNSMRGGLPPREGRGMPPPLRGGPGGPGGPGGPMGRMG 170	Ş
b 1155 1183	밁
Y 55 TLDDLADFFKQCGVVKMNKRTGQPMIHIYLDKETGKPKGDATVSYEDPPTAKAAVEWFDG 114	8
1104 GERGYTGSAGEKGEPGPPGSEGLPGPPGPAGPRGERGPQG	망
1 GGRGGMGSAGERGGFNKPGGPMDEGPDL	१
Query Match 13.8%; Score 265; DB 4; Length 1603; Best Local Similarity 29.6%; Pred. No. 2.2e-13; Matches 113; Conservative 14; Mismatches 125; Indels 130; Gaps 19;	M B Q
ORGANISM: Human S-09-949-016-6136	us-c
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6136	Ω
NUMBER OF SEQ ID NOS: 207012 . SOFTWARE: FastSEQ for Windows Version 4.0	
APPLICATION N FILING DATE:	 m m
PRIOR APPLICATION NUMBER: 60/237, 768 PRIOR FILING DATE: 2000-10-03	
FILING DATE: 2000-10-20	
FILING DATE: 2000-0	
CURRENT APPLICATION NUMBER: US/09/949,016	
96	
ANT: VENTER, J. Craig et al. OF INVENTION: POLYMORPHISMS IN KNOWN GENES	
GENERAL INFORMATION:	 GH 8
-09-94	US-0
ROTT TO 1.5	R FIST
b 871 PHGHRPHDVPGHRGHDHRGPPPHEHRGHDGPGH-GGGGHR 909	밁
y 303 PPGPIMEQMGGRRG	Ş
B11 GHRPHEGPGGGISGGSGHRPHEGPGGGMCAGGGHRPHEGPGGSMGGSGGHRPHEGPGHGG 870	망
y 259 GLMDRGGPGGMFRGGRGGDRGGFRGGRGMDRGGFGGGR-RGGPGG 302	ş
b 770 EGPGGGMGNSSGHRPHEGPGGGMGSGHRPHEGPGGSMGGGG 810	망
205 QCPNPGCGNQNFAWRTECNQCKAPKP-EGFLPPPFPPPPGGDRGRGGPGGMRGGRG 258	Ş
5 710 GPGPGPGPYHRGRGGRGGNEPPPPPPPPRGARGGRSGGPPNGRGGPGGGMVGGGGHRPH 769	망
158	Ş
657 HFPPGPGGPMPGPHGGPGGPVGPRLLGPPPPPRGGDPFWDGPGDPMRGGPMRG 709	망
100 EDPPTAKAAVEWFDGKDFQGSKLKVSLARKKPPMNSMRGGLPPREGRGMPPP	ş

Search completed: February 18, 2005, 15:31:22 Job time : 47 secs